

PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 478
ID ACD85415 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 479
ID ACD86029 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 480
ID ACF76025 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 481
ID ACF60925 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 482
ID ACH05812 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 483
ID ADA82956 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 484
ID ACF56071 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068680-A1.

PD 10-APR-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 485
ID ACF55457 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 486
ID ADB86264 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 487
ID ACF56378 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 488
ID ACF56685 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 489
ID ACF55764 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 490
ID ACF55150 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 491
ID ADD05994 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 492
ID ADG02989 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 493
ID ADG01696 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 494
ID ADF95871 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 495
ID ADG12686 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 496
ID ADH09346 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 497
ID ABX78788 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2003027272-A1.
PD 06-FEB-2003..
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 498
ID ACA75760 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 499
ID ACA71240 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 500
ID ACC87768 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 501
ID ACC87154 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 502
ID ACD04327 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 503
ID ACA69658 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 504
ID ACA90503 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 505
ID ACC89610 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 506
ID ACA98401 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 507
ID ACA94043 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 508
ID ACD15436 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 509
ID ACD09023 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 510
ID ACC96943 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 511
ID ACF15664 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 512
ID ACAT3031 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 513
ID ACD03203 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 514
ID ACD02018 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 515
ID ACA92210 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 516
ID ADL33125 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 11; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 517
ID ADM30661 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 11; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 518
ID ADE74658 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 6.2%; Score 143.2; DB 12; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 519
ID ADE75270 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 6.2%; Score 143.2; DB 12; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 520
ID ADF96483 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 6.2%; Score 143.2; DB 12; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 521
ID ADG04754 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 12; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 522
ID ADG00914 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 12; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 523

ID ADG83170 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 524

ID ADH26451 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 525

ID ADH33420 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 526

ID ADJ55159 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 527

ID ADL06423 standard; cDNA; 2974 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3.
PN WO2004016225-A2.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 528

ID ADJ64930 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 529

ID ADM31826 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 530

ID ADM36873 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 12; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 531
ID ADM40678 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 12; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 532
ID ADN38286 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 12; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 533
ID ADP72670 standard; DNA; 1858 BP.
DE Renal toxin progression gene marker #1259.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
 Query Match 6.1%; Score 142; DB 12; Length 1858;
 Best Local Similarity 51.3%; Pred. No. 9.6e-31;
RESULT 534
ID ABN75524 standard; cDNA; 336 BP.
DE Human ORF471 cDNA, SEQ ID NO:941.
PN WO200190366-A2.
PD 29-NOV-2001.
PA (CURA-) CURAGEN CORP.
 Query Match 6.1%; Score 141.8; DB 6; Length 336;
 Best Local Similarity 65.9%; Pred. No. 3.5e-31;
RESULT 535
ID ADB53826 standard; DNA; 1947 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4368.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
 Query Match... 6.1%; Score 141.8; DB 10; Length 1947;
 Best Local Similarity 48.1%; Pred. No. 1.1e-30;
RESULT 536
ID ABT42419 standard; DNA; 1947 BP.
DE Toxicity modelling related rat gene SEQ ID No 2121.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
 Query Match 6.1%; Score 141.8; DB 10; Length 1947;
 Best Local Similarity 48.1%; Pred. No. 1.1e-30;
RESULT 537
ID ADP72852 standard; DNA; 1947 BP.

DE Renal toxin progression gene marker #1441.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 6.1%; Score 141.8; DB 12; Length 1947;
Best Local Similarity 48.1%; Pred. No. 1.1e-30;
RESULT 538
ID ABX72195 standard; cDNA; 1705 BP.
DE Human NOVX polynucleotide #26.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 141.6; DB 8; Length 1705;
Best Local Similarity 48.2%; Pred. No. 1.2e-30;
RESULT 539
ID AAD59158 standard; cDNA; 1620 BP.
DE Human UDP-glucuronosyltransferase cDNA #2.
PN US2003073105-A1.
PD 17-APR-2003.
PA (LASE/) LASEK A K W.
PA (SORN/) SORNASSE T.
Query Match 6.1%; Score 141.2; DB 10; Length 1620;
Best Local Similarity 48.8%; Pred. No. 1.5e-30;
RESULT 540
ID ABX72194 standard; cDNA; 3050 BP.
DE Human NOVX polynucleotide #25.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 141; DB 8; Length 3050;
Best Local Similarity 48.2%; Pred. No. 2.6e-30;
RESULT 541
ID ADB58614 standard; DNA; 1593 BP.
DE Toxicity-related gene, SEQ ID 3640.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 6.0%; Score 140; DB 10; Length 1593;
Best Local Similarity 51.2%; Pred. No. 3.4e-30;
RESULT 542
ID ADB53262 standard; DNA; 1593 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3804.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 6.0%; Score 140; DB 10; Length 1593;
Best Local Similarity 51.2%; Pred. No. 3.4e-30;
RESULT 543
ID ABT42206 standard; DNA; 1593 BP.
DE Toxicity modelling related rat gene SEQ ID No 1908.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 6.0%; Score 140; DB 10; Length 1593;
Best Local Similarity 51.2%; Pred. No. 3.4e-30;
RESULT 544
ID AAL41490 standard; DNA; 1639 BP.

DE Drug metabolising enzyme encoding DNA - 7493833CB1.
PN WO200266654-A2.
PD 29-AUG-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.0%; Score 139.8; DB 6; Length 1639;
Best Local Similarity 49.2%; Pred. No. 4e-30;
RESULT 545
ID ADA11075 standard; cDNA; 1714 BP.
DE Human cDNA differentially expressed in colon cancer #138.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
Query Match 6.0%; Score 139.2; DB 9; Length 1714;
Best Local Similarity 49.8%; Pred. No. 6.2e-30;
RESULT 546
ID ABL68501 standard; DNA; 1855 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6838.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 6.0%; Score 139.2; DB 6; Length 1855;
Best Local Similarity 49.8%; Pred. No. 6.6e-30;
RESULT 547
ID ABL68868 standard; DNA; 1855 BP.
DE Kidney cancer related gene sequence SEQ ID NO:7205.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 6.0%; Score 139.2; DB 6; Length 1855;
Best Local Similarity 49.8%; Pred. No. 6.6e-30;
RESULT 548
ID ABN95622 standard; DNA; 1855 BP.
DE Gene #2120 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 6.0%; Score 139.2; DB 6; Length 1855;
Best Local Similarity 49.8%; Pred. No. 6.6e-30;
RESULT 549
ID ADD71099 standard; DNA; 1855 BP.
DE Human UDP glycosyltransferase 2 family B7 gene SEQ ID NO:103.
PN WO2003061564-A2.
PD 31-JUL-2003.
PA (GENE-) GENE LOGIC INC.
PA (LGBI-) LG BIOMEDICAL INST.
Query Match 6.0%; Score 139.2; DB 10; Length 1855;
Best Local Similarity 49.8%; Pred. No. 6.6e-30;
RESULT 550
ID ADR46644 standard; DNA; 1855 BP.
DE Cancer-associated protein coding sequence, SEQ ID 57.
PN WO2004073657-A2.
PD 02-SEP-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.0%; Score 139.2; DB 13; Length 1855;
Best Local Similarity 49.8%; Pred. No. 6.6e-30;
RESULT 551

ID AAD45991 standard; cDNA; 1991 BP.
DE Human UGT2B7 cDNA.
PN WO200259375-A2.
PD 01-AUG-2002.
PA (UYCH-) UNIV CHICAGO.
 Query Match 6.0%; Score 139.2; DB 6; Length 1991;
 Best Local Similarity 49.8%; Pred. No. 6.9e-30;
RESULT 552
ID ADP72910 standard; DNA; 1846 BP.
DE Renal toxin progression gene marker #1499.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
 Query Match 5.9%; Score 136.8; DB 12; Length 1846;
 Best Local Similarity 50.9%; Pred. No. 3.4e-29;
RESULT 553
ID ADP72818 standard; DNA; 1844 BP.
DE Renal toxin progression gene marker #1407.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
 Query Match 5.9%; Score 136.4; DB 12; Length 1844;
 Best Local Similarity 48.6%; Pred. No. 4.5e-29;
RESULT 554
ID AAV15900 standard; cDNA; 2107 BP.
DE Uridine diphospho-glucuronosyltransferase 2B17 (UGT2B17) encoding cDNA.
PN WO9744466-A1.
PD 27-NOV-1997.
PA (ENDO-) ENDORECHERCHE INC.
 Query Match 5.9%; Score 136.4; DB 2; Length 2107;
 Best Local Similarity 49.5%; Pred. No. 4.9e-29;
RESULT 555
ID ADR07753 standard; cDNA; 2172 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1259.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 5.9%; Score 136.4; DB 13; Length 2172;
 Best Local Similarity 48.0%; Pred. No. 5e-29;
RESULT 556
ID AAS78773 standard; cDNA; 2448 BP.
DE DNA encoding novel human diagnostic protein #14577.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
 Query Match 5.9%; Score 136.4; DB 5; Length 2448;
 Best Local Similarity 48.0%; Pred. No. 5.4e-29;
RESULT 557
ID AAS78611 standard; cDNA; 2448 BP.
DE DNA encoding novel human diagnostic protein #14415.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
 Query Match 5.9%; Score 136.4; DB 5; Length 2448;
 Best Local Similarity 48.0%; Pred. No. 5.4e-29;
RESULT 558
ID AAS84057 standard; cDNA; 2448 BP.

DE DNA encoding novel human diagnostic protein #19861.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
 Query Match 5.9%; Score 136.4; DB 5; Length 2448;
 Best Local Similarity 48.0%; Pred. No. 5.4e-29;
RESULT 559
ID AAS74393 standard; cDNA; 2448 BP.
DE DNA encoding novel human diagnostic protein #10197.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
 Query Match 5.9%; Score 136.4; DB 5; Length 2448;
 Best Local Similarity 48.0%; Pred. No. 5.4e-29;
RESULT 560
ID AAS72022 standard; cDNA; 2448 BP.
DE DNA encoding novel human diagnostic protein #7826.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
 Query Match 5.9%; Score 136.4; DB 5; Length 2448;
 Best Local Similarity 48.0%; Pred. No. 5.4e-29;
RESULT 561
ID ABL67995 standard; DNA; 2448 BP.
DE Ovary cancer related gene sequence SEQ ID NO:6332.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
 Query Match 5.9%; Score 136.4; DB 6; Length 2448;
 Best Local Similarity 48.0%; Pred. No. 5.4e-29;
RESULT 562
ID ACA89932 standard; cDNA; 2448 BP.
DE Gene differentially regulated in cardiovascular disease #53.
PN WO2003031650-A2.
PD 17-APR-2003.
PA (FARB) BAYER AG.
 Query Match 5.9%; Score 136.4; DB 8; Length 2448;
 Best Local Similarity 48.0%; Pred. No. 5.4e-29;
RESULT 563
ID AAZ95200 standard; DNA; 1854 BP.
DE Human UDP-glucuronosyltransferase 2B7 nucleotide sequence.
PN WO200006776-A1.
PD 10-FEB-2000.
PA (AXYS-) AXYS PHARM INC.
 Query Match 5.9%; Score 136; DB 3; Length 1854;
 Best Local Similarity 49.6%; Pred. No. 5.9e-29;
RESULT 564
ID ADC39064 standard; cDNA; 3005 BP.
DE Novel human NOVX polypeptide coding sequence SEQ ID NO: 3.
PN WO2003010327-A2.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
 Query Match 5.8%; Score 135.4; DB 10; Length 3005;
 Best Local Similarity 48.4%; Pred. No. 1.2e-28;
RESULT 565
ID AAC65396 standard; cDNA; 1650 BP.
DE Human carbohydrate-modifying enzyme cDNA Incyte ID No: 2912330CB1.

PN WO200063351-A2.
PD 26-OCT-2000.
PA (INCY-) INCYTE GENOMICS INC.
 Query Match 5.8%; Score 133.8; DB 3; Length 1650;
 Best Local Similarity 49.3%; Pred. No. 2.5e-28;
RESULT 566
ID ADR25043 standard; DNA; 1894 BP.
DE Breast cancer prognosis marker #904.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
 Query Match 5.8%; Score 133.8; DB 13; Length 1894;
 Best Local Similarity 49.1%; Pred. No. 2.7e-28;
RESULT 567
ID ADG47988 standard; DNA; 1756 BP.
DE Human UDP-glucuronosyl transferase (UGT) gene.
PN US2003101002-A1.
PD 29-MAY-2003.
PA (BART/) BARTHA G T.
PA (WALK/) WALKER M.
 Query Match 5.8%; Score 133.4; DB 12; Length 1756;
 Best Local Similarity 48.7%; Pred. No. 3.4e-28;
RESULT 568
ID AAS91380 standard; cDNA; 1766 BP.
DE DNA encoding novel human diagnostic protein #27184.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
 Query Match 5.8%; Score 133.4; DB 5; Length 1766;
 Best Local Similarity 48.7%; Pred. No. 3.4e-28;
RESULT 569
ID ADE53677 standard; cDNA; 1829 BP.
DE Human prostate cancer cDNA #24.
PN US2003190640-A1.
PD 09-OCT-2003.
PA (FARI/) FARIS M.
PA (PEAR/) PEARSON C I.
 Query Match 5.7%; Score 133.2; DB 10; Length 1829;
 Best Local Similarity 49.3%; Pred. No. 4e-28;
RESULT 570
ID ADO42268 standard; cDNA; 1662 BP.
DE Human NOVX polynucleotide #59.
PN US2004058338-A1.
PD 25-MAR-2004.
PA (AGEE/) AGEE M L.
PA (ALSO/) ALSOBOOK J P.
PA (ANDE/) ANDERSON D W.
PA (BERG/) BERGHS C.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CATT/) CATTERTON E.
PA (DIPPI/) DIPPIPPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (GANG/) GANGOLLI E A.

PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (ROTH/) ROTHBERG B G.
PA (GUOX/) GUO X S.
PA (HERR/) HERRMANN J L.
PA (HALV/) HALVORSEN Y.
PA (JIWW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MILL/) MILLER C E.
PA (ORTT/) ORT T.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.

Query Match 5.7%; Score 133; DB 12; Length 1662;
Best Local Similarity 47.7%; Pred. No. 4.3e-28;

RESULT 571

ID ADR19685 standard; DNA; 1614 BP.
DE Human drug metabolising enzyme (DME)-6 gene sequence.

PN WO200226988-A2.
PD 04-APR-2002.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 5.7%; Score 132; DB 7; Length 1614;
Best Local Similarity 48.4%; Pred. No. 8.4e-28;

RESULT 572

ID AAD57503 standard; cDNA; 1608 BP.
DE Human enzyme (ENZM) cDNA #15.

PN WO2003052075-A2.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 5.7%; Score 131.6; DB 9; Length 1608;
Best Local Similarity 49.2%; Pred. No. 1.1e-27;

RESULT 573

ID ADB58692 standard; DNA; 1846 BP.
DE Toxicity-related gene, SEQ ID 3718.

PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.

Query Match 5.7%; Score 131.6; DB 10; Length 1846;
Best Local Similarity 48.4%; Pred. No. 1.2e-27;

RESULT 574

ID ADB53380 standard; DNA; 1846 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3922.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
 Query Match 5.7%; Score 131.6; DB 10; Length 1846;
 Best Local Similarity 48.4%; Pred. No. 1.2e-27;
RESULT 575
ID ADP72819 standard; DNA; 1846 BP.
DE Renal toxin progression gene marker #1408.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
 Query Match 5.7%; Score 131.6; DB 12; Length 1846;
 Best Local Similarity 48.4%; Pred. No. 1.2e-27;
RESULT 576
ID AAZ95199 standard; DNA; 2092 BP.
DE Human UDP-glucuronosyltransferase 2B4 nucleotide sequence.
PN WO200006776-A1.
PD 10-FEB-2000.
PA (AXYS-) AXYS PHARM INC.
 Query Match 5.7%; Score 131.6; DB 3; Length 2092;
 Best Local Similarity 49.2%; Pred. No. 1.3e-27;
RESULT 577
ID ABN96789 standard; DNA; 2123 BP.
DE Gene #3287 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
 Query Match 5.6%; Score 130; DB 6; Length 2123;
 Best Local Similarity 49.1%; Pred. No. 4e-27;
RESULT 578
ID AAD06860 standard; DNA; 1722 BP.
DE Human breast cancer specific gene-2 (BCSG-2) #2.
PN WO200137779-A2.
PD 31-MAY-2001.
PA (DIAD-) DIADEXUS INC.
 Query Match 5.6%; Score 129; DB 5; Length 1722;
 Best Local Similarity 48.0%; Pred. No. 6.9e-27;
RESULT 579
ID ABN97261 standard; DNA; 2799 BP.
DE Gene #3759 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
 Query Match 5.6%; Score 129; DB 6; Length 2799;
 Best Local Similarity 48.0%; Pred. No. 9.6e-27;
RESULT 580
ID ADD71006 standard; DNA; 2799 BP.
DE Human UDP glycosyltransferase 2 family B10 gene SEQ ID NO:10.
PN WO2003061564-A2.
PD 31-JUL-2003.
PA (GENE-) GENE LOGIC INC.
PA (LGBI-) LG BIOMEDICAL INST.
 Query Match 5.6%; Score 129; DB 10; Length 2799;
 Best Local Similarity 48.0%; Pred. No. 9.6e-27;
RESULT 581

ID ADO00385 standard; cDNA; 1593 BP.
DE Novel human cDNA sequence #1200.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 5.5%; Score 128.4; DB 12; Length 1593;
Best Local Similarity 49.0%; Pred. No. 1e-26;
RESULT 582

ID ADN98816 standard; cDNA; 1593 BP.
DE Novel human cDNA sequence #416.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 5.5%; Score 128.4; DB 12; Length 1593;
Best Local Similarity 49.0%; Pred. No. 1e-26;
RESULT 583

ID AAZ95206 standard; DNA; 1976 BP.
DE Human UDP-glucuronosyltransferase 2B15 nucleotide sequence.
PN WO200006776-A1.
PD 10-FEB-2000.
PA (AXYS-) AXYS PHARM INC.
Query Match 5.5%; Score 128.4; DB 3; Length 1976;
Best Local Similarity 49.0%; Pred. No. 1.1e-26;
RESULT 584

ID ABK84210 standard; cDNA; 2090 BP.
DE Human cDNA differentially expressed in granulocytic cells #781.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 5.5%; Score 128.4; DB 6; Length 2090;
Best Local Similarity 49.0%; Pred. No. 1.2e-26;
RESULT 585

ID ABN96795 standard; DNA; 2090 BP.
DE Gene #3293 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 5.5%; Score 128.4; DB 6; Length 2090;
Best Local Similarity 49.0%; Pred. No. 1.2e-26;
RESULT 586

ID ABT17080 standard; DNA; 2090 BP.
DE Androgen-independent prostate cancer-related DNA - SEQ ID No 11.
PN WO200298358-A2.
PD 12-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.5%; Score 128.4; DB 8; Length 2090;
Best Local Similarity 49.0%; Pred. No. 1.2e-26;
RESULT 587

ID AAD43928 standard; cDNA; 1413 BP.
DE Human UDP-glycosyltransferase cDNA.
PN US6383789-B1.
PD 07-MAY-2002.
PA (PEKE) PE CORP NY.
Query Match 5.5%; Score 127.6; DB 6; Length 1413;
Best Local Similarity 50.1%; Pred. No. 1.6e-26;
RESULT 588

ID ADE48040 standard; cDNA; 1413 BP.

DE Human UDP-glycosyltransferase protein cDNA.
PN US2002182692-A1.
PD 05-DEC-2002.
PA (PEKE) PE CORP NY.
Query Match 5.5%; Score 127.6; DB 12; Length 1413;
Best Local Similarity 50.1%; Pred. No. 1.6e-26;
RESULT 589
ID ADQ14303 standard; cDNA; 1413 BP.
DE Human UDP-glycosyltransferase cDNA.
PN US2004132089-A1.
PD 08-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 5.5%; Score 127.6; DB 12; Length 1413;
Best Local Similarity 50.1%; Pred. No. 1.6e-26;
RESULT 590
ID ADA10927 standard; cDNA; 2150 BP.
DE Human cDNA differentially expressed in colon cancer #31.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
Query Match 5.5%; Score 127.2; DB 9; Length 2150;
Best Local Similarity 49.6%; Pred. No. 2.8e-26;
RESULT 591
ID ADE53678 standard; cDNA; 2150 BP.
DE Human prostate cancer cDNA #25.
PN US2003190640-A1.
PD 09-OCT-2003.
PA (FARI/) FARIS M.
PA (PEAR/) PEARSON C I.
Query Match 5.5%; Score 127.2; DB 10; Length 2150;
Best Local Similarity 49.6%; Pred. No. 2.8e-26;
RESULT 592
ID AAS69710 standard; cDNA; 1859 BP.
DE DNA encoding novel human diagnostic protein #5514.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 126.4; DB 5; Length 1859;
Best Local Similarity 48.8%; Pred. No. 4.4e-26;
RESULT 593
ID AAS69711 standard; cDNA; 2802 BP.
DE DNA encoding novel human diagnostic protein #5515.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 125.4; DB 5; Length 2802;
Best Local Similarity 47.7%; Pred. No. 1.1e-25;
RESULT 594
ID ABN97347 standard; DNA; 2093 BP.
DE Gene #3845 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 5.4%; Score 125.2; DB 6; Length 2093;
Best Local Similarity 48.7%; Pred. No. 1.1e-25;
RESULT 595

ID ADH13736 standard; DNA; 1045 BP.
DE Human ENZM enzyme gene sequence SeqID89.
PN WO2003093439-A2.
PD 13-NOV-2003.
PA (INCY-) INCYTE CORP.
 Query Match 5.4%; Score 124.8; DB 12; Length 1045;
 Best Local Similarity 49.6%; Pred. No. 8.9e-26;
RESULT 596

ID ADC14292 standard; DNA; 1356 BP.
DE Human enzyme ENZM-45 gene.
PN WO2003042357-A2.
PD 22-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
 Query Match 5.4%; Score 124.8; DB 10; Length 1356;
 Best Local Similarity 49.6%; Pred. No. 1.1e-25;
RESULT 597

ID AAD06844 standard; DNA; 1713 BP.
DE Human breast cancer specific gene-2 (BCSG-2) #1.
PN WO200137779-A2.
PD 31-MAY-2001.
PA (DIAD-) DIADEXUS INC.
 Query Match 5.4%; Score 124.4; DB 5; Length 1713;
 Best Local Similarity 48.3%; Pred. No. 1.6e-25;
RESULT 598

ID ACN91984 standard; DNA; 2844 BP.
DE Breast cancer related marker, seq id 13134.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 5.4%; Score 124.2; DB 11; Length 2844;
 Best Local Similarity 48.4%; Pred. No. 2.6e-25;
RESULT 599

ID ADA10965 standard; cDNA; 1889 BP.
DE Human cDNA differentially expressed in colon cancer #56.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
 Query Match 5.3%; Score 124; DB 9; Length 1889;
 Best Local Similarity 48.7%; Pred. No. 2.3e-25;
RESULT 600

ID ADA11071 standard; cDNA; 1712 BP.
DE Human cDNA differentially expressed in colon cancer #135.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/). LASEK A W.
PA (JONE/) JONES D A.
 Query Match 5.28%; Score 121.2; DB 9; Length 1712;
 Best Local Similarity 48.1%; Pred. No. 1.5e-24;
RESULT 601

ID AAD59155 standard; cDNA; 1712 BP.
DE Human UDP-glucuronosyltransferase 2B cDNA.
PN US2003073105-A1.
PD 17-APR-2003.
PA (LASE/) LASEK A K W.
PA (SORN/) SORNASSE T.
 Query Match 5.2%; Score 121.2; DB 10; Length 1712;

Best Local Similarity 48.1%; Pred. No. 1.5e-24;
RESULT 602
ID ADR19693 standard; DNA; 1224 BP.
DE Human drug metabolising enzyme (DME)-14 gene sequence.
PN WO200226988-A2.
PD 04-APR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.2%; Score 120.6; DB 7; Length 1224;
Best Local Similarity 49.8%; Pred. No. 1.8e-24;
RESULT 603
ID AAS69712 standard; cDNA; 2111 BP.
DE DNA encoding novel human diagnostic protein #5516.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.2%; Score 120.6; DB 5; Length 2111;
Best Local Similarity 49.1%; Pred. No. 2.6e-24;
RESULT 604
ID ABX63845 standard; cDNA; 2349 BP.
DE Human cDNA #845 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Query Match 5.2%; Score 119.6; DB 8; Length 2349;
Best Local Similarity 47.7%; Pred. No. 5.5e-24;
RESULT 605
ID ADA11033 standard; cDNA; 2349 BP.
DE Human cDNA differentially expressed in colon cancer #106.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
Query Match 5.2%; Score 119.6; DB 9; Length 2349;
Best Local Similarity 47.7%; Pred. No. 5.5e-24;
RESULT 606
ID ABZ23121 standard; DNA; 2351 BP.
DE Nucleotide sequence of an UDP-glucuronosyltransferase-1.
PN WO200286074-A2.
PD 31-OCT-2002.
PA (MINU) UNIV MINNESOTA.
PA (STEE/) STEER C J.
PA (KREN/) KREN B T.
PA (LINE/) LINEHAN-STIEERS C.
PA (MCIV/) MCIVOR S R.
PA (HACK/) HACKETT P B.
PA (BELU/) BELUR S....
Query Match 5.2%; Score 119.6; DB 8; Length 2351;
Best Local Similarity 47.7%; Pred. No. 5.5e-24;
RESULT 607
ID ACF62731 standard; DNA; 2351 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:659.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 5.2%; Score 119.6; DB 8; Length 2351;
Best Local Similarity 47.7%; Pred. No. 5.5e-24;
RESULT 608

ID ADB20846 standard; DNA; 2351 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:659.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 5.2%; Score 119.6; DB 8; Length 2351;
Best Local Similarity 47.7%; Pred. No. 5.5e-24;
RESULT 609
ID ADB87935 standard; DNA; 2351 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:659.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 5.2%; Score 119.6; DB 10; Length 2351;
Best Local Similarity 47.7%; Pred. No. 5.5e-24;
RESULT 610
ID ADB96918 standard; DNA; 2351 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:659.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 5.2%; Score 119.6; DB 10; Length 2351;
Best Local Similarity 47.7%; Pred. No. 5.5e-24;
RESULT 611
ID ADB92109 standard; DNA; 2351 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:659.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 5.2%; Score 119.6; DB 10; Length 2351;
Best Local Similarity 47.7%; Pred. No. 5.5e-24;
RESULT 612
ID ADH13719 standard; DNA; 1097 BP.
DE Human ENZM enzyme gene sequence SeqID72.
PN WO2003093439-A2.
PD 13-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 5.1%; Score 119.2; DB 12; Length 1097;
Best Local Similarity 50.0%; Pred. No. 4.3e-24;
RESULT 613
ID ABL68883 standard; DNA; 2422 BP.
DE Kidney cancer related gene sequence SEQ ID NO:7220.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 5.0%; Score 115.8; DB 6; Length 2422;
Best Local Similarity 49.1%; Pred. No. 7.6e-23;
RESULT 614
ID ABN95608 standard; DNA; 2422 BP.
DE Gene #2106 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 5.0%; Score 115.8; DB 6; Length 2422;
Best Local Similarity 49.1%; Pred. No. 7.6e-23;
RESULT 615
ID AAQ27369 standard; cDNA; 2351 BP.

DE HUG-Brl.
PN WO9212987-A1.
PD 06-AUG-1992.
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
Query Match 5.0%; Score 115; DB 2; Length 2351;
Best Local Similarity 47.5%; Pred. No. 1.3e-22;
RESULT 616
ID ADC14256 standard; DNA; 1816 BP.
DE Human enzyme ENZM-9 gene.
PN WO2003042357-A2.
PD 22-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.9%; Score 114.6; DB 10; Length 1816;
Best Local Similarity 47.1%; Pred. No. 1.4e-22;
RESULT 617
ID ADK70323 standard; cDNA; 2366 BP.
DE Respiratory disease differentially expressed cDNA #59.
PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 4.9%; Score 112.8; DB 12; Length 2366;
Best Local Similarity 48.6%; Pred. No. 5.9e-22;
RESULT 618
ID ABX63816 standard; cDNA; 2380 BP.
DE Human cDNA #816 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Query Match 4.9%; Score 112.8; DB 8; Length 2380;
Best Local Similarity 48.6%; Pred. No. 5.9e-22;
RESULT 619
ID ADA11035 standard; cDNA; 2385 BP.
DE Human cDNA differentially expressed in colon cancer #107.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
Query Match 4.9%; Score 112.8; DB 9; Length 2385;
Best Local Similarity 48.6%; Pred. No. 5.9e-22;
RESULT 620
ID ABA99240 standard; DNA; 2320 BP.
DE Human UGT1A9 encoding sequence #1.
PN US2002016293-A1.
PD 07-FEB-2002.
PA (RATA/) RATAIN M J.
PA (INNO/) INNOCENTI F.
PA (IYER/) IYER L.
Query Match 4.8%; Score 111.4; DB 6; Length 2320;
Best Local Similarity 48.4%; Pred. No. 1.5e-21;
RESULT 621
ID ABA99241 standard; DNA; 2320 BP.
DE Human UGT1A9 encoding sequence #2.
PN US2002016293-A1.
PD 07-FEB-2002.
PA (RATA/) RATAIN M J.
PA (INNO/) INNOCENTI F.
PA (IYER/) IYER L.

Query Match 4.8%; Score 111.4; DB 6; Length 2320;
Best Local Similarity 48.4%; Pred. No. 1.5e-21;
RESULT 622
ID ABA05198 standard; cDNA; 2320 BP.
DE Human uridine 5'diphosphate glucuronyltransferase UGT1A9 cDNA #1.
PN WO200180896-A2.
PD 01-NOV-2001.
PA (ARCH-) ARCH DEV CORP.
Query Match 4.8%; Score 111.4; DB 6; Length 2320;
Best Local Similarity 48.4%; Pred. No. 1.5e-21;
RESULT 623
ID ABA05199 standard; cDNA; 2320 BP.
DE Human uridine 5'diphosphate glucuronyltransferase UGT1A9 cDNA #2.
PN WO200180896-A2.
PD 01-NOV-2001.
PA (ARCH-) ARCH DEV CORP.
Query Match 4.8%; Score 111.4; DB 6; Length 2320;
Best Local Similarity 48.4%; Pred. No. 1.5e-21;
RESULT 624
ID AAD30177 standard; DNA; 2320 BP.
DE Human UDP-glucuronosyl transferase (UGT1A9) gene exon 1.
PN WO200206523-A2.
PD 24-JAN-2002.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 4.8%; Score 111.4; DB 6; Length 2320;
Best Local Similarity 48.4%; Pred. No. 1.5e-21;
RESULT 625
ID ADM72569 standard; DNA; 2585 BP.
DE Nucleotide sequence of UGT allele UGT1A9*1.
PN WO2004027088-A2.
PD 01-APR-2004.
PA (UYLA-) UNIV LAVAL.
Query Match 4.8%; Score 111.4; DB 12; Length 2585;
Best Local Similarity 48.4%; Pred. No. 1.6e-21;
RESULT 626
ID ADM72571 standard; DNA; 2585 BP.
DE Nucleotide sequence of UGT allele UGT1A9*3.
PN WO2004027088-A2.
PD 01-APR-2004.
PA (UYLA-) UNIV LAVAL.
Query Match 4.8%; Score 111.4; DB 12; Length 2585;
Best Local Similarity 48.4%; Pred. No. 1.6e-21;
RESULT 627
ID ADM72570 standard; DNA; 2585 BP.
DE Nucleotide sequence of UGT allele UGT1A9*2.
PN WO2004027088-A2.
PD 01-APR-2004.
PA (UYLA-) UNIV LAVAL.
Query Match 4.8%; Score 111.4; DB 12; Length 2585;
Best Local Similarity 48.4%; Pred. No. 1.6e-21;
RESULT 628
ID AAS81804 standard; cDNA; 2220 BP.
DE DNA encoding novel human diagnostic protein #17608.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.8%; Score 111.2; DB 5; Length 2220;

Best Local Similarity 79.9%; Pred. No. 1.7e-21;
RESULT 629
ID AAS91252 standard; cDNA; 1655 BP.
DE DNA encoding novel human diagnostic protein #27056.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.8%; Score 111; DB 5; Length 1655;
Best Local Similarity 48.7%; Pred. No. 1.6e-21;
RESULT 630
ID ACN89671 standard; DNA; 811 BP.
DE Breast cancer related marker, seq id 10821.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.7%; Score 110; DB 11; Length 811;
Best Local Similarity 53.9%; Pred. No. 2e-21;
RESULT 631
ID ABL11505 standard; cDNA; 1584 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28997.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.4%; Score 101.6; DB 4; Length 1584;
Best Local Similarity 47.6%; Pred. No. 1e-18;
RESULT 632
ID ABL11504 standard; cDNA; 3650 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28994.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.4%; Score 101.6; DB 4; Length 3650;
Best Local Similarity 47.6%; Pred. No. 1.7e-18;
RESULT 633
ID AAQ27370 standard; cDNA; 2368 BP.
DE HUG-Br2.
PN WO9212987-A1.
PD 06-AUG-1992.
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
Query Match 4.3%; Score 100.6; DB 2; Length 2368;
Best Local Similarity 47.9%; Pred. No. 2.6e-18;
RESULT 634
ID ABL18781 standard; DNA; 1212 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 7816.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.3%; Score 98.8; DB 4; Length 1212;
Best Local Similarity 49.4%; Pred. No. 5.7e-18;
RESULT 635
ID ADS96565 standard; cDNA; 1587 BP.
DE Drosophila melanogaster protein coding sequence, SEQ ID 186.
PN WO2004039999-A2.
PD 13-MAY-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.3%; Score 98.8; DB 13; Length 1587;
Best Local Similarity 47.2%; Pred. No. 6.9e-18;

RESULT 636

ID ABL20593 standard; DNA; 1704 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 13252.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 4.3%; Score 98.8; DB 4; Length 1704;
Best Local Similarity 47.2%; Pred. No. 7.2e-18;

RESULT 637

ID ABL18780 standard; DNA; 3212 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 7813.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 4.3%; Score 98.8; DB 4; Length 3212;
Best Local Similarity 49.4%; Pred. No. 1.1e-17;

RESULT 638

ID ABL20592 standard; DNA; 4357 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 13249.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 4.3%; Score 98.8; DB 4; Length 4357;
Best Local Similarity 47.2%; Pred. No. 1.3e-17;

RESULT 639

ID ABL14299 standard; cDNA; 1458 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 37379.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 4.2%; Score 97.6; DB 4; Length 1458;
Best Local Similarity 46.2%; Pred. No. 1.5e-17;

RESULT 640

ID ABL14298 standard; cDNA; 3458 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 37376.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 4.2%; Score 97.6; DB 4; Length 3458;
Best Local Similarity 46.2%; Pred. No. 2.6e-17;

RESULT 641

ID ADB58853 standard; DNA; 1593 BP.
DE Toxicity-related gene, SEQ ID 3879.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.

Query Match 4.2%; Score 97; DB 10; Length 1593;
Best Local Similarity 47.7%; Pred. No. 2.4e-17;

RESULT 642

ID ADB53570 standard; DNA; 1593 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4112.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.

Query Match 4.2%; Score 97; DB 10; Length 1593;
Best Local Similarity 47.7%; Pred. No. 2.4e-17;

RESULT 643

ID ABT42362 standard; DNA; 1593 BP.
DE Toxicity modelling related rat gene SEQ ID No 2064.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 4.2%; Score 97; DB 10; Length 1593;
Best Local Similarity 47.7%; Pred. No. 2.4e-17;
RESULT 644
ID ADP72524 standard; DNA; 1593 BP.
DE Renal toxin progression gene marker #1113.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 4.2%; Score 97; DB 12; Length 1593;
Best Local Similarity 47.7%; Pred. No. 2.4e-17;
RESULT 645
ID AAZ45118 standard; DNA; 735 BP.
DE UDP-glucuronosyltransferase 1 (UGT1) exons 2-5 nucleotide sequence.
PN WO9957322-A2.
PD 11-NOV-1999.
PA (AXYS-) AXYS PHARM INC.
Query Match 4.1%; Score 95.6; DB 3; Length 735;
Best Local Similarity 50.2%; Pred. No. 3.7e-17;
RESULT 646
ID ADP72545 standard; DNA; 1927 BP.
DE Renal toxin progression gene marker #1134.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 4.1%; Score 95.4; DB 12; Length 1927;
Best Local Similarity 47.5%; Pred. No. 8.1e-17;
RESULT 647
ID ABL11511 standard; cDNA; 1560 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29015.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 93.4; DB 4; Length 1560;
Best Local Similarity 50.8%; Pred. No. 2.8e-16;
RESULT 648
ID ABL11510 standard; cDNA; 3828 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29012.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 93.4; DB 4; Length 3828;
Best Local Similarity 50.8%; Pred. No. 5e-16;
RESULT 649
ID ACN45086 standard; DNA; 54493 BP.
DE Human genomic sequence hCG37578.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.0%; Score 93.2; DB 11; Length 54493;
Best Local Similarity 79.1%; Pred. No. 3.4e-15;
RESULT 650
ID ABL07443 standard; cDNA; 1652 BP.

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16811.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 93; DB 4; Length 1652;
Best Local Similarity 49.7%; Pred. No. 3.8e-16;
RESULT 651
ID ABL07442 standard; cDNA; 3991 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16808.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 93; DB 4; Length 3991;
Best Local Similarity 49.7%; Pred. No. 6.8e-16;
RESULT 652
ID ABL15252 standard; cDNA; 14112 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40238.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 93; DB 4; Length 14112;
Best Local Similarity 49.7%; Pred. No. 1.6e-15;
RESULT 653
ID ABT09061 standard; DNA; 662 BP.
DE Phase-1 Rat CT gene SEQ ID No 149.
PN WO200266682-A2.
PD 29-AUG-2002.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 4.0%; Score 92.8; DB 6; Length 662;
Best Local Similarity 50.4%; Pred. No. 2.4e-16;
RESULT 654
ID ADR91345 standard; cDNA; 662 BP.
DE Spleen necrosis predictive cDNA sequence, SEQ ID No 301.
PN WO2004083402-A2.
PD 30-SEP-2004.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 4.0%; Score 92.8; DB 13; Length 662;
Best Local Similarity 50.4%; Pred. No. 2.4e-16;
RESULT 655
ID ABT09603 standard; DNA; 642 BP.
DE Phase-1 Rat CT gene SEQ ID No 691.
PN WO200266682-A2.
PD 29-AUG-2002.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 4.0%; Score 91.8; DB 6; Length 642;
Best Local Similarity 50.4%; Pred. No. 4.6e-16;
RESULT 656
ID ADG45772 standard; DNA; 642 BP.
DE Liver inflammatory predictive gene related DNA sequence.
PN WO2003095624-A2.
PD 20-NOV-2003.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 4.0%; Score 91.8; DB 12; Length 642;
Best Local Similarity 50.4%; Pred. No. 4.6e-16;
RESULT 657
ID ADH23038 standard; DNA; 642 BP.
DE Partial DNA sequence of a rat kidney toxicity predictive gene (366).

PN WO2003100030-A2.
PD 04-DEC-2003.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 4.0%; Score 91.8; DB 12; Length 642;
Best Local Similarity 50.4%; Pred. No. 4.6e-16;
RESULT 658
ID ABT09349 standard; DNA; 662 BP.
DE Phase-1 Rat CT gene SEQ ID No 437.
PN WO200266682-A2.
PD 29-AUG-2002.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 3.9%; Score 91.6; DB 6; Length 662;
Best Local Similarity 50.5%; Pred. No. 5.4e-16;
RESULT 659
ID ABL26823 standard; DNA; 1648 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 31942.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 91; DB 4; Length 1648;
Best Local Similarity 46.0%; Pred. No. 1.5e-15;
RESULT 660
ID AAD57526 standard; cDNA; 2526 BP.
DE Human enzyme (ENZM) cDNA #38.
PN WO2003052075-A2.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.9%; Score 90.6; DB 9; Length 2526;
Best Local Similarity 49.6%; Pred. No. 2.6e-15;
RESULT 661
ID ADH13757 standard; DNA; 2602 BP.
DE Human ENZM enzyme gene sequence SeqID110.
PN WO2003093439-A2.
PD 13-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 3.8%; Score 89.2; DB 12; Length 2602;
Best Local Similarity 49.3%; Pred. No. 7e-15;
RESULT 662
ID ABL27914 standard; DNA; 5278 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35215.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.8%; Score 88.8; DB 4; Length 5278;
Best Local Similarity 47.6%; Pred. No. 1.5e-14;
RESULT 663
ID ADP72573 standard; DNA; 2484 BP.
DE Renal toxin progression gene marker #1162.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 3.8%; Score 88.2; DB 12; Length 2484;
Best Local Similarity 47.8%; Pred. No. 1.4e-14;
RESULT 664
ID AAD57521 standard; cDNA; 2491 BP.
DE Human enzyme (ENZM) cDNA #33.
PN WO2003052075-A2.

PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.8%; Score 88; DB 9; Length 2491;
Best Local Similarity 49.8%; Pred. No. 1.6e-14;
RESULT 665
ID ABL11161 standard; cDNA; 1595 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 27965.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.8%; Score 87.4; DB 4; Length 1595;
Best Local Similarity 45.9%; Pred. No. 1.7e-14;
RESULT 666
ID ABX44475 standard; cDNA; 419 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #9640.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.7%; Score 86.2; DB 8; Length 419;
Best Local Similarity 55.6%; Pred. No. 1.6e-14;
RESULT 667
ID ABL01468 standard; DNA; 874 BP.
DE Murine apoptosis related DNA sequence #133.
PN DE10126344-A1.
PD 24-JAN-2002.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 3.7%; Score 86.2; DB 6; Length 874;
Best Local Similarity 49.2%; Pred. No. 2.7e-14;
RESULT 668
ID ABL30082 standard; DNA; 3716 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41719.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.7%; Score 85.2; DB 4; Length 3716;
Best Local Similarity 46.0%; Pred. No. 1.4e-13;
RESULT 669
ID ABL28713 standard; DNA; 1572 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37612.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.6%; Score 82.6; DB 4; Length 1572;
Best Local Similarity 48.1%; Pred. No. 4.7e-13;
RESULT 670
ID ABL28712 standard; DNA; 3572 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37609.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.6%; Score 82.6; DB 4; Length 3572;
Best Local Similarity 48.1%; Pred. No. 8.1e-13;
RESULT 671
ID ABL11160 standard; cDNA; 4016 BP.

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 27962.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.5%; Score 80.8; DB 4; Length 4016;
Best Local Similarity 47.9%; Pred. No. 3e-12;
RESULT 672
ID ABL29221 standard; DNA; 1593 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 39136.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.5%; Score 80.6; DB 4; Length 1593;
Best Local Similarity 49.5%; Pred. No. 1.9e-12;
RESULT 673
ID ABL29220 standard; DNA; 3659 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 39133.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.5%; Score 80.6; DB 4; Length 3659;
Best Local Similarity 49.5%; Pred. No. 3.3e-12;
RESULT 674
ID ABL28205 standard; DNA; 1413 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 36088.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.4%; Score 79.4; DB 4; Length 1413;
Best Local Similarity 48.4%; Pred. No. 3.9e-12;
RESULT 675
ID ABL27915 standard; DNA; 2820 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35218.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.4%; Score 79.4; DB 4; Length 2820;
Best Local Similarity 49.0%; Pred. No. 6.2e-12;
RESULT 676
ID ABT09604 standard; DNA; 678 BP.
DE Phase-1 Rat CT gene SEQ ID NO 692.
PN WO200266682-A2.
PD 29-AUG-2002.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 3.4%; Score 78.6; DB 6; Length 678;
Best Local Similarity 49.4%; Pred. No. 4.2e-12;
RESULT 677
ID ABL26822 standard; DNA; 5205 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 31939.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.4%; Score 77.8; DB 4; Length 5205;
Best Local Similarity 58.4%; Pred. No. 2.8e-11;
RESULT 678
ID ABX48695 standard; cDNA; 426 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #13860.

PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.3%; Score 76.8; DB 8; Length 426;
Best Local Similarity 49.0%; Pred. No. 1.1e-11;
RESULT 679
ID ABX44899 standard; cDNA; 418 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #10064.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.3%; Score 75.8; DB 8; Length 418;
Best Local Similarity 52.8%; Pred. No. 2.1e-11;
RESULT 680
ID ABK63527 standard; cDNA; 603 BP.
DE Rat sequence differentially expressed in response to a hepatotoxin #1434.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.2%; Score 74.6; DB 6; Length 603;
Best Local Similarity 48.3%; Pred. No. 6.1e-11;
RESULT 681
ID ADP72781 standard; DNA; 603 BP.
DE Renal toxin progression gene marker #1370.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 3.2%; Score 74.6; DB 12; Length 603;
Best Local Similarity 48.3%; Pred. No. 6.1e-11;
RESULT 682
ID ABL78475 standard; cDNA; 582 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:1453.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 3.2%; Score 74; DB 6; Length 582;
Best Local Similarity 61.3%; Pred. No. 9e-11;
RESULT 683
ID AAS91382 standard; cDNA; 2406 BP.
DE DNA encoding novel human diagnostic protein #27186.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.2%; Score 73.4; DB 5; Length 2406;
Best Local Similarity 48.4%; Pred. No. 3.5e-10;
RESULT 684
ID AAL19612 standard; cDNA; 293 BP.
DE Human breast cancer expressed polynucleotide 12069.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 3.1%; Score 72; DB 4; Length 293;
Best Local Similarity 60.9%; Pred. No. 2.3e-10;
RESULT 685
ID AAL10032 standard; cDNA; 439 BP.
DE Human breast cancer expressed polynucleotide 2489.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.1%; Score 72; DB 4; Length 439;
Best Local Similarity 60.9%; Pred. No. 2.9e-10;
RESULT 686
ID ACN80231 standard; DNA; 450 BP.
DE Breast cancer related marker, seq id 1381.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.1%; Score 72; DB 11; Length 450;
Best Local Similarity 60.9%; Pred. No. 3e-10;
RESULT 687
ID ABK63526 standard; cDNA; 601 BP.
DE Rat sequence differentially expressed in response to a hepatotoxin #1433.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.1%; Score 70.8; DB 6; Length 601;
Best Local Similarity 48.1%; Pred. No. 8.3e-10;
RESULT 688
ID ADP72780 standard; DNA; 601 BP.
DE Renal toxin progression gene marker #1369.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 3.1%; Score 70.8; DB 12; Length 601;
Best Local Similarity 48.1%; Pred. No. 8.3e-10;
RESULT 689
ID ABL11455 standard; cDNA; 1680 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28847.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.0%; Score 69.4; DB 4; Length 1680;
Best Local Similarity 45.5%; Pred. No. 4.3e-09;
RESULT 690
ID ABL11471 standard; cDNA; 1782 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28895.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.0%; Score 69.4; DB 4; Length 1782;
Best Local Similarity 44.3%; Pred. No. 4.5e-09;
RESULT 691
ID ABL11454 standard; cDNA; 3741 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28844.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.0%; Score 69.4; DB 4; Length 3741;

Best Local Similarity 45.5%; Pred. No. 7.3e-09;
RESULT 692
ID ABL11470 standard; cDNA; 3849 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28892.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.0%; Score 69.4; DB 4; Length 3849;
Best Local Similarity 44.3%; Pred. No. 7.4e-09;
RESULT 693
ID ABX36904 standard; cDNA; 350 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #2069.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.0%; Score 69.2; DB 8; Length 350;
Best Local Similarity 58.1%; Pred. No. 1.7e-09;
RESULT 694
ID ABX36905 standard; cDNA; 381 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #2070.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.0%; Score 69.2; DB 8; Length 381;
Best Local Similarity 58.1%; Pred. No. 1.8e-09;
RESULT 695
ID ABL08183 standard; cDNA; 1491 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19031.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.0%; Score 69.2; DB 4; Length 1491;
Best Local Similarity 56.0%; Pred. No. 4.6e-09;
RESULT 696
ID ABL08182 standard; cDNA; 3784 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19028.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.0%; Score 69.2; DB 4; Length 3784;
Best Local Similarity 56.0%; Pred. No. 8.4e-09;
RESULT 697
ID ABL29264 standard; DNA; 3595 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 39265.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.0%; Score 68.6; DB 4; Length 3595;
Best Local Similarity 48.6%; Pred. No. 1.2e-08;
RESULT 698
ID ABL29265 standard; DNA; 1539 BP.

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 39268.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
 Query Match 2.9%; Score 68; DB 4; Length 1539;
 Best Local Similarity 51.4%; Pred. No. 1.1e-08;
RESULT 699
ID AAS81103 standard; cDNA; 2602 BP.
DE DNA encoding novel human diagnostic protein #16907.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
 Query Match 2.9%; Score 67.2; DB 5; Length 2602;
 Best Local Similarity 57.7%; Pred. No. 2.6e-08;
RESULT 700
ID AAS91381 standard; cDNA; 2602 BP.
DE DNA encoding novel human diagnostic protein #27185.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
 Query Match 2.9%; Score 67.2; DB 5; Length 2602;
 Best Local Similarity 57.7%; Pred. No. 2.6e-08;
RESULT 701
ID AAS92577 standard; cDNA; 2602 BP.
DE DNA encoding novel human diagnostic protein #28381.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
 Query Match 2.9%; Score 67.2; DB 5; Length 2602;
 Best Local Similarity 57.7%; Pred. No. 2.6e-08;
RESULT 702
ID ABX47071 standard; cDNA; 416 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12236.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
 Query Match 2.9%; Score 66.8; DB 8; Length 416;
 Best Local Similarity 55.6%; Pred. No. 1e-08;
RESULT 703
ID ABL26825 standard; DNA; 1931 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 31948.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
 Query Match 2.9%; Score 66.2; DB 4; Length 1931;
 Best Local Similarity 48.1%; Pred. No. 4.3e-08;
RESULT 704
ID ABL18375 standard; DNA; 1188 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 6598.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
 Query Match 2.8%; Score 66; DB 4; Length 1188;
 Best Local Similarity 47.9%; Pred. No. 3.5e-08;

RESULT 705

ID ABL18374 standard; DNA; 3188 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 6595.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.8%; Score 66; DB 4; Length 3188;
Best Local Similarity 47.9%; Pred. No. 6.8e-08;

RESULT 706

ID ABL19473 standard; DNA; 1672 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 9892.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.8%; Score 65.8; DB 4; Length 1672;
Best Local Similarity 45.8%; Pred. No. 5.1e-08;

RESULT 707

ID ABL19472 standard; DNA; 3751 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 9889.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.8%; Score 65.8; DB 4; Length 3751;
Best Local Similarity 45.8%; Pred. No. 8.7e-08;

RESULT 708

ID ABL18869 standard; DNA; 1488 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 8080.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.8%; Score 65.4; DB 4; Length 1488;
Best Local Similarity 60.3%; Pred. No. 6.2e-08;

RESULT 709

ID ABL26827 standard; DNA; 1584 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 31954.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.8%; Score 65.4; DB 4; Length 1584;
Best Local Similarity 60.3%; Pred. No. 6.5e-08;

RESULT 710

ID ABX74515 standard; cDNA; 1977 BP.
DE Human cDNA sequence #58 down-regulated in CC-RCC patients.
PN WO200279411-A2.
PD 10-OCT-2002.
PA (VAND-) VAN ANDEL INST.

Query Match 2.8%; Score 65.4; DB 10; Length 1977;
Best Local Similarity 58.5%; Pred. No. 7.5e-08;

RESULT 711

ID ABL16660 standard; DNA; 3613 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1453.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.8%; Score 65.4; DB 4; Length 3613;
Best Local Similarity 60.3%; Pred. No. 1.1e-07;

RESULT 712

ID ABL26826 standard; DNA; 4082 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 31951.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.8%; Score 65.4; DB 4; Length 4082;
Best Local Similarity 60.3%; Pred. No. 1.2e-07;
RESULT 713

ID ABL18868 standard; DNA; 4082 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 8077.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.8%; Score 65.4; DB 4; Length 4082;
Best Local Similarity 60.3%; Pred. No. 1.2e-07;
RESULT 714

ID ABL16191 standard; DNA; 1623 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 46.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.8%; Score 64.6; DB 4; Length 1623;
Best Local Similarity 52.4%; Pred. No. 1.1e-07;
RESULT 715

ID ABL16190 standard; DNA; 3683 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 43.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.8%; Score 64.6; DB 4; Length 3683;
Best Local Similarity 52.4%; Pred. No. 2e-07;
RESULT 716

ID AAA87473 standard; DNA; 259 BP.
DE Rat hepatocyte carcinogenesis biomarker nucleic acid SEQ ID NO:397.
PN WO200044902-A2.
PD 03-AUG-2000.
PA (SEAR) SEARLE & CO G D.
Query Match 2.8%; Score 64.4; DB 3; Length 259;
Best Local Similarity 53.1%; Pred. No. 3.9e-08;
RESULT 717

ID AAI17431 standard; DNA; 500 BP.
DE Probe #7364 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.8%; Score 63.8; DB 4; Length 500;
Best Local Similarity 60.8%; Pred. No. 9e-08;
RESULT 718

ID ABA62357 standard; DNA; 500 BP.
DE Human foetal liver single exon nucleic acid probe #10662.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.8%; Score 63.8; DB 4; Length 500;
Best Local Similarity 60.8%; Pred. No. 9e-08;
RESULT 719

ID AAI42337 standard; DNA; 500 BP.

DE Probe #11023 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.8%; Score 63.8; DB 4; Length 500;
Best Local Similarity 60.8%; Pred. No. 9e-08;
RESULT 720
ID ABA29697 standard; DNA; 500 BP.
DE Probe #8163 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.8%; Score 63.8; DB 4; Length 500;
Best Local Similarity 60.8%; Pred. No. 9e-08;
RESULT 721
ID AAK36579 standard; DNA; 500 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 11136.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.8%; Score 63.8; DB 4; Length 500;
Best Local Similarity 60.8%; Pred. No. 9e-08;
RESULT 722
ID AAK10692 standard; DNA; 500 BP.
DE Human brain expressed single exon probe SEQ ID NO: 10683.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.8%; Score 63.8; DB 4; Length 500;
Best Local Similarity 60.8%; Pred. No. 9e-08;
RESULT 723
ID ABS36232 standard; DNA; 500 BP.
DE Human liver single exon probe, SEQ ID No 11222.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.8%; Score 63.8; DB 4; Length 500;
Best Local Similarity 60.8%; Pred. No. 9e-08;
RESULT 724
ID AAZ95197 standard; DNA; 689 BP.
DE Human UGT2B4 exon 5 nucleotide sequence.
PN WO200006776-A1.
PD 10-FEB-2000.
PA (AXYS-) AXYS PHARM INC.
Query Match 2.8%; Score 63.8; DB 3; Length 689;
Best Local Similarity 60.8%; Pred. No. 1.1e-07;
RESULT 725
ID ABL15269 standard; cDNA; 1521 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40289.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.8%; Score 63.8; DB 4; Length 1521;
Best Local Similarity 46.3%; Pred. No. 1.9e-07;
RESULT 726
ID ABL15268 standard; cDNA; 3576 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40286.

PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.8%; Score 63.8; DB 4; Length 3576;
Best Local Similarity 46.3%; Pred. No. 3.3e-07;
RESULT 727
ID ABX38071 standard; cDNA; 370 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3236.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.7%; Score 63.6; DB 8; Length 370;
Best Local Similarity 54.8%; Pred. No. 8.5e-08;
RESULT 728
ID ABX36135 standard; cDNA; 378 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #1300.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.7%; Score 63.4; DB 8; Length 378;
Best Local Similarity 56.5%; Pred. No. 9.9e-08;
RESULT 729
ID ADT97393 standard; cDNA; 396 BP.
DE Colon cancer associated human cDNA sequence #2900.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 2.7%; Score 63.4; DB 11; Length 396;
Best Local Similarity 53.1%; Pred. No. 1e-07;
RESULT 730
ID ABK12423 standard; DNA; 21000 BP.
DE cDNA encoding human drug-metabolising enzyme.
PN WO200218554-A2.
PD 07-MAR-2002.
PA (APPL-) APPLERA CORP.
Query Match 2.7%; Score 63.4; DB 6; Length 21000;
Best Local Similarity 58.9%; Pred. No. 1.4e-06;
RESULT 731
ID AAZ07208 standard; cDNA; 391 BP.
DE Human lung tumour protein LT86-5 cDNA sequence.
PN WO9938973-A2.
PD 05-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match 2.7%; Score 62.4; DB 2; Length 391;
Best Local Similarity 54.3%; Pred. No. 2e-07;
RESULT 732
ID AAC79066 standard; cDNA; 391 BP.
DE Human lung tumour-specific cDNA #21.
PN WO200060077-A2.
PD 12-OCT-2000.
PA (CORI-) CORIXA CORP.

Query Match 2.7%; Score 62.4; DB 3; Length 391;
Best Local Similarity 54.3%; Pred. No. 2e-07;
RESULT 733

ID AAD23141 standard; cDNA; 391 BP.
DE Human lung tumour-specific protein LT86-5 cDNA.
PN WO200172295-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.

Query Match 2.7%; Score 62.4; DB 4; Length 391;
Best Local Similarity 54.3%; Pred. No. 2e-07;
RESULT 734

ID ADD67078 standard; cDNA; 391 BP.
DE Human lung tumour-specific cDNA sequence, SEQ ID No 21.
PN WO200292001-A2.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.

Query Match 2.7%; Score 62.4; DB 10; Length 391;
Best Local Similarity 54.3%; Pred. No. 2e-07;
RESULT 735

ID ADE87583 standard; cDNA; 391 BP.
DE Human lung tumour antigen cDNA #21.
PN US2003118599-A1.
PD 26-JUN-2003.
PA (CORI-) CORIXA CORP.

Query Match 2.7%; Score 62.4; DB 10; Length 391;
Best Local Similarity 54.3%; Pred. No. 2e-07;
RESULT 736

ID ABX45859 standard; cDNA; 417 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11024.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.

Query Match 2.7%; Score 62.4; DB 8; Length 417;
Best Local Similarity 57.8%; Pred. No. 2.1e-07;
RESULT 737

ID ABL17155 standard; DNA; 1443 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 2938.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.7%; Score 62.2; DB 4; Length 1443;
Best Local Similarity 45.4%; Pred. No. 5.5e-07;
RESULT 738

ID AAZ95204 standard; DNA; 1591 BP.
DE Human UGT2B7 exon 4 nucleotide sequence.
PN WO200006776-A1.
PD 10-FEB-2000.
PA (AXYS-) AXYS PHARM INC.

Query Match 2.7%; Score 62.2; DB 3; Length 1591;
Best Local Similarity 60.2%; Pred. No. 5.9e-07;
RESULT 739

ID ABL17154 standard; DNA; 3495 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 2935.
PN WO200171042-A2.

PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.7%; Score 62.2; DB 4; Length 3495;
Best Local Similarity 45.4%; Pred. No. 9.9e-07;
RESULT 740
ID ADB58891 standard; DNA; 2301 BP.
DE Toxicity-related gene, SEQ ID 3917.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 62; DB 10; Length 2301;
Best Local Similarity 46.7%; Pred. No. 8.6e-07;
RESULT 741
ID ADB53607 standard; DNA; 2301 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4149.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 62; DB 10; Length 2301;
Best Local Similarity 46.7%; Pred. No. 8.6e-07;
RESULT 742
ID ABZ83776 standard; cDNA; 1024 BP.
DE Toxicologically relevant human nucleotide sequence #935.
PN WO2003016500-A2.
PD 27-FEB-2003.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 2.7%; Score 61.8; DB 10; Length 1024;
Best Local Similarity 48.2%; Pred. No. 5.7e-07;
RESULT 743
ID ABL07575 standard; cDNA; 1527 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17207.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.7%; Score 61.8; DB 4; Length 1527;
Best Local Similarity 46.1%; Pred. No. 7.5e-07;
RESULT 744
ID ABL07574 standard; cDNA; 4647 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17204.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.7%; Score 61.8; DB 4; Length 4647;
Best Local Similarity 46.1%; Pred. No. 1.6e-06;
RESULT 745
ID ABL16192 standard; DNA; 3679 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 49.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.6%; Score 61.4; DB 4; Length 3679;
Best Local Similarity 51.7%; Pred. No. 1.8e-06;
RESULT 746
ID ABL30083 standard; DNA; 1500 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41722.
PN WO200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Query Match 2.6%; Score 60.4; DB 4; Length..1500;
Best Local Similarity 47.8%; Pred. No. 1.9e-06;
RESULT 747
ID ABX37848 standard; cDNA; 196 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3013.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 60.2; DB 8; Length 196;
Best Local Similarity 57.8%; Pred. No. 5.8e-07;
RESULT 748
ID AAI26647 standard; DNA; 220 BP.
DE Probe #16580 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.6%; Score 60; DB 4; Length 220;
Best Local Similarity 60.4%; Pred. No. 7.1e-07;
RESULT 749
ID ABA74889 standard; DNA; 220 BP.
DE Human foetal liver single exon nucleic acid probe #23194.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.6%; Score 60; DB 4; Length 220;
Best Local Similarity 60.4%; Pred. No. 7.1e-07;
RESULT 750
ID AAI55416 standard; DNA; 220 BP.
DE Probe #24102 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.6%; Score 60; DB 4; Length 220;
Best Local Similarity 60.4%; Pred. No. 7.1e-07;
RESULT 751
ID ABA39585 standard; DNA; 220 BP.
DE Probe #18051 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.6%; Score 60; DB 4; Length 220;
Best Local Similarity 60.4%; Pred. No. 7.1e-07;
RESULT 752
ID AAK49539 standard; DNA; 220 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 24096.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.6%; Score 60; DB 4; Length 220;
Best Local Similarity 60.4%; Pred. No. 7.1e-07;
RESULT 753
ID AAK23383 standard; DNA; 220 BP.
DE Human brain expressed single exon probe SEQ ID NO: 23374.

PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 2.6%; Score 60; DB 4; Length 220;
 Best Local Similarity 60.4%; Pred. No. 7.1e-07;
RESULT 754
ID ABS49158 standard; DNA; 220 BP.
DE Human liver single exon probe, SEQ ID No 24148.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 2.6%; Score 60; DB 4; Length 220;
 Best Local Similarity 60.4%; Pred. No. 7.1e-07;
RESULT 755
ID ABL11493 standard; cDNA; 1668 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28961.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
 Query Match 2.6%; Score 59.6; DB 4; Length 1668;
 Best Local Similarity 50.9%; Pred. No. 3.6e-06;
RESULT 756
ID ABL11492 standard; cDNA; 3740 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28958.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
 Query Match 2.6%; Score 59.6; DB 4; Length 3740;
 Best Local Similarity 50.9%; Pred. No. 6.2e-06;
RESULT 757
ID ABN85391 standard; DNA; 1606 BP.
DE Human NOV13, glucuronosyltransferase-like protein, coding sequence.
PN WO200255704-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
 Query Match 2.6%; Score 59.4; DB 6; Length 1606;
 Best Local Similarity 48.6%; Pred. No. 4e-06;
RESULT 758
ID ADI16615 standard; cDNA; 1606 BP.
DE Human NOVX cDNA to treat human pathological conditions SeqID151.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
 Query Match 2.6%; Score 59.4; DB 6; Length 1606;
 Best Local Similarity 48.6%; Pred. No. 4e-06;
RESULT 759.
ID ADN42269 standard; cDNA; 1606 BP.
DE Human cDNA encoding NOV 40.
PN US2004033493-A1.
PD 19-FEB-2004.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (GANG/) GANGOLLI E A.

PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELLI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENA/) PENA C E A.
PA (FURT/) FURTAK K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSO BROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.

Query Match 2.6%; Score 59.4; DB 12; Length 1606;
Best Local Similarity 48.6%; Pred. No. 4e-06;

RESULT 760

ID ABA63293 standard; DNA; 589 BP.
DE Human foetal liver single exon nucleic acid probe #11598.

PN WO200157277-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 2.5%; Score 59; DB 4; Length 589;
Best Local Similarity 59.1%; Pred. No. 2.7e-06;

RESULT 761

ID ABS37187 standard; DNA; 589 BP.

DE Human liver single exon probe, SEQ ID No 12177.

PN WO200157273-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 2.5%; Score 59; DB 4; Length 589;
Best Local Similarity 59.1%; Pred. No. 2.7e-06;

RESULT 762

ID ADT97647 standard; cDNA; 432 BP.

DE Colon cancer associated human cDNA sequence #3154.

PN US2003087818-A1.

PD 08-MAY-2003.

PA (CORI-) CORIXA CORP.

Query Match 2.5%; Score 58.2; DB 11; Length 432;
Best Local Similarity 51.0%; Pred. No. 3.9e-06;

RESULT 763

ID AAD57513 standard; cDNA; 1465 BP.

DE Human enzyme (ENZM) cDNA #25.

PN WO2003052075-A2.

PD 26-JUN-2003.

PA (INCY-) INCYTE GENOMICS INC.

Query Match 2.5%; Score 58.2; DB 9; Length 1465;
Best Local Similarity 52.6%; Pred. No. 8.7e-06;

RESULT 764

ID ABL08287 standard; cDNA; 2036 BP.

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19343.

PN WO200171042-A2.

PD 27-SEP-2001.

PA (PEKE) PE CORP NY.

Query Match 2.5%; Score 57.4; DB 4; Length 2036;

Best Local Similarity 44.9%; Pred. No. 1.9e-05;
RESULT 765
ID ABL08286 standard; cDNA; 4386 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19340.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.5%; Score 57.4; DB 4; Length 4386;
Best Local Similarity 44.9%; Pred. No. 3.1e-05;
RESULT 766
ID AAT10106 standard; cDNA to mRNA; 1731 BP.
DE Maize UDP-glucose indol-3-yl:acetyl:glucosyl transferase sequence.
PN WO9600291-A1.
PD 04-JAN-1996.
PA (RESE) RESEARCH CORP TECHNOLOGIES INC.
Query Match 2.4%; Score 56.8; DB 2; Length 1731;
Best Local Similarity 60.3%; Pred. No. 2.5e-05;
RESULT 767
ID AAH51495 standard; DNA; 983 BP.
DE Human UGT2B4 related DNA containing a biallelic polymorphism SEQ ID 386.
PN WO200058508-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 2.4%; Score 56.2; DB 3; Length 983;
Best Local Similarity 53.4%; Pred. No. 2.6e-05;
RESULT 768
ID ABL26824 standard; DNA; 4966 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 31945.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.4%; Score 56.2; DB 4; Length 4966;
Best Local Similarity 50.2%; Pred. No. 7.7e-05;
RESULT 769
ID AAC03286 standard; cDNA; 350 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 3284.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 2.4%; Score 55.8; DB 3; Length 350;
Best Local Similarity 53.7%; Pred. No. 1.7e-05;
RESULT 770
ID ABZ83269 standard; cDNA; 1024 BP.
DE Toxicologically relevant human nucleotide sequence #428.
PN WO2003016500-A2.
PD 27-FEB-2003.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 2.4%; Score 55.6; DB 10; Length 1024;
Best Local Similarity 48.7%; Pred. No. 4.1e-05;
RESULT 771
ID ABA75736 standard; DNA; 203 BP.
DE Human foetal liver single exon nucleic acid probe #24041.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.4%; Score 55.2; DB 4; Length 203;
Best Local Similarity 58.5%; Pred. No. 1.8e-05;

RESULT 772

ID ABS50023 standard; DNA; 203 BP.
DE Human liver single exon probe, SEQ ID No 25013.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.4%; Score 55.2; DB 4; Length 203;
Best Local Similarity 58.5%; Pred. No. 1.8e-05;

RESULT 773

ID AAZ95210 standard; DNA; 1602 BP.
DE Human UGT2B15 exon 4 nucleotide sequence.
PN WO200006776-A1.
PD 10-FEB-2000.
PA (AXYS-) AXYS PHARM INC.
Query Match 2.4%; Score 55; DB 3; Length 1602;
Best Local Similarity 61.5%; Pred. No. 8.3e-05;

RESULT 774

ID AAD55028 standard; DNA; 1380 BP.
DE Alstroemeria UDP-glucosyltransferase homologue gene, k7.
PN WO2002101013-A2.
PD 19-DEC-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PRAB/) PRABHU V.
Query Match 2.3%; Score 54.2; DB 10; Length 1380;
Best Local Similarity 58.3%; Pred. No. 0.00013;

RESULT 775

ID ABL28204 standard; DNA; 3642 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 36085.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.3%; Score 54.2; DB 4; Length 3642;
Best Local Similarity 58.3%; Pred. No. 0.00025;

RESULT 776

ID ADJ12064 standard; DNA; 531 BP.
DE Maize cDNA modulated by post-transcriptional gene silencing SeqID 700.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
Query Match 2.3%; Score 53.8; DB 11; Length 531;
Best Local Similarity 57.4%; Pred. No. 9.1e-05;

RESULT 777

ID AAD55029 standard; DNA; 1380 BP.
DE Alstroemeria UDP-glucosyltransferase homologue gene, e12.
PN WO2002101013-A2.
PD 19-DEC-2002.

PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PRAB/) PRABHU V.
Query Match 2.3%; Score 53.8; DB 10; Length 1380;
Best Local Similarity 57.4%; Pred. No. 0.00017;
RESULT 778
ID ACH80037 standard; DNA; 577 BP.
DE Human genome derived single exon probe #13232.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 2.3%; Score 53.4; DB 12; Length 577;
Best Local Similarity 51.9%; Pred. No. 0.00013;
RESULT 779
ID AAQ33026 standard; DNA; 775 BP.
DE Exons 3-4 from the UGT1 gene locus.
PN WO9212987-A1.
PD 06-AUG-1992.
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
Query Match 2.3%; Score 53.4; DB 2; Length 775;
Best Local Similarity 51.9%; Pred. No. 0.00015;
RESULT 780
ID AAD30179 standard; DNA; 784 BP.
DE Human UDP-glucuronosyl transferase (UGT1A) gene exon 4.
PN WO200206523-A2.
PD 24-JAN-2002.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 2.3%; Score 53.4; DB 6; Length 784;
Best Local Similarity 51.9%; Pred. No. 0.00016;
RESULT 781
ID ABL16193 standard; DNA; 1620 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 52.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.3%; Score 53.4; DB 4; Length 1620;
Best Local Similarity 57.5%; Pred. No. 0.00025;
RESULT 782
ID AAS18543 standard; DNA; 18887 BP.
DE DNA encoding UDP glycosyltransferase 1 (UGT1A1).
PN WO200179230-A2.
PD 25-OCT-2001.
PA (GENA-) GENAISANCE PHARM INC.
Query Match 2.3%; Score 53.4; DB 6; Length 18887;
Best Local Similarity 51.9%; Pred. No. 0.0013;
RESULT 783
ID AAA87255 standard; DNA; 223 BP.
DE Rat hepatocyte carcinogenesis biomarker nucleic acid SEQ ID NO:179.
PN WO200044902-A2.
PD 03-AUG-2000.
PA (SEAR) SEARLE & CO G D.
Query Match 2.3%; Score 53.2; DB 3; Length 223;
Best Local Similarity 63.9%; Pred. No. 7.7e-05;
RESULT 784
ID ABX43094 standard; cDNA; 393 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #8259.

PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.3%; Score 53.2; DB 8; Length 393;
Best Local Similarity 50.5%; Pred. No. 0.00011;
RESULT 785
ID ABX36148 standard; cDNA; 383 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #1313.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.3%; Score 52.8; DB 8; Length 383;
Best Local Similarity 52.2%; Pred. No. 0.00015;
RESULT 786
ID AAL61198 standard; DNA; 1209 BP.
DE Actinosynnema pretiosum glycosyltransferase gene.
PN WO2003045312-A2.
PD 05-JUN-2003.
PA (UNIW) UNIV WASHINGTON.
Query Match 2.3%; Score 52.6; DB 8; Length 1209;
Best Local Similarity 62.6%; Pred. No. 0.00036;
RESULT 787
ID AAL61224 standard; DNA; 82746 BP.
DE Actinosynnema pretiosum ansamitocin biosynthetic gene cluster I.
PN WO2003045312-A2.
PD 05-JUN-2003.
PA (UNIW) UNIV WASHINGTON.
Query Match 2.3%; Score 52.6; DB 8; Length 82746;
Best Local Similarity 62.6%; Pred. No. 0.0059;
RESULT 788
ID ABV24713 standard; cDNA; 707 BP.
DE Human prostate expression marker cDNA 24704.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.2%; Score 52; DB 5; Length 707;
Best Local Similarity 54.2%; Pred. No. 0.00038;
RESULT 789
ID ADK56220 standard; DNA; 691 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #3603..
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 2.2%; Score 51; DB 10; Length 691;
Best Local Similarity 60.4%; Pred. No. 0.00074;
RESULT 790
ID ADA69456 standard; DNA; 1494 BP.
DE Rice gene, SEQ ID 2779.
PN WO2003000898-A1.
PD 03-JAN-2003.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.2%; Score 50.4; DB 8; Length 1494;
Best Local Similarity 61.4%; Pred. No. 0.0019;
RESULT 791
ID ADC25968 standard; cDNA; 1536 BP.
DE Eucalyptus grandis UDP-glucosyltransferase cDNA.
PN WO2003066836-A2.
PD 14-AUG-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 2.2%; Score 50.4; DB 10; Length 1536;
Best Local Similarity 57.7%; Pred. No. 0.0019;
RESULT 792
ID ADC25973 standard; cDNA; 1575 BP.
DE Eucalyptus grandis UDP-glucosyltransferase cDNA variant.
PN WO2003066836-A2.
PD 14-AUG-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 2.2%; Score 50.4; DB 10; Length 1575;
Best Local Similarity 57.7%; Pred. No. 0.0019;
RESULT 793
ID ABX78354 standard; cDNA; 1601 BP.
DE Rice stress response protein cDNA.
PN US2002152497-A1.
PD 17-OCT-2002.
PA (FALC/) FALCO S C.
PA (FAMO/) FAMODU O O.
PA (MEYE/) MEYERS B C.
PA (MIAO/) MIAO G.
PA (ODEL/) ODELL J T.
PA (RAFA/) RAFALSKI J A.
PA (THOR/) THORPE C J.
PA (SAKA/) SAKAI H.
PA (WENG/) WENG Z.
Query Match 2.2%; Score 50.4; DB 10; Length 1601;
Best Local Similarity 61.4%; Pred. No. 0.002;
RESULT 794
ID ADC08517 standard; DNA; 1999 BP.
DE Rice DNA sequence Seq ID822 related to grain filling.
PN WO2003000905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.2%; Score 50.4; DB 10; Length 1999;
Best Local Similarity 49.8%; Pred. No. 0.0023;
RESULT 795
ID ADF29092 standard; DNA; 131680 BP.
DE Agrotis segetum granulovirus genomic DNA sequence, SEQ ID NO:1.
PN CN1381581-A.
PD 27-NOV-2002.
PA (JIKA-) JIKANG BIOTECHNOLOGY CO LTD SHANGHAI.
Query Match 2.2%; Score 50.4; DB 10; Length 131680;
Best Local Similarity 48.1%; Pred. No. 0.037;
RESULT 796
ID ADJ11499 standard; DNA; 627 BP.
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 135.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.

PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
Query Match 2.2%; Score 50.2; DB 11; Length 627;
Best Local Similarity 50.2%; Pred. No. 0.0012;
RESULT 797
ID ADP87526 standard; DNA; 1628 BP.
DE Japanese morning glory flavanon 3-hydroxylase DNA.
PN JP2004180592-A.
PD 02-JUL-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 2.1%; Score 49.8; DB 12; Length 1628;
Best Local Similarity 57.3%; Pred. No. 0.003;
RESULT 798
ID ABX78352 standard; cDNA; 398 BP.
DE Corn stress response protein EST #10.
PN US2002152497-A1.
PD 17-OCT-2002.
PA (FALC/) FALCO S C.
PA (FAMO/) FAMODU O O.
PA (MEYE/) MEYERS B C.
PA (MIAO/) MIAO G.
PA (ODEL/) ODELL J T.
PA (RAFA/) RAFALSKI J A.
PA (THOR/) THORPE C J.
PA (SAKA/) SAKAI H.
PA (WENG/) WENG Z.
Query Match 2.1%; Score 49.6; DB 10; Length 398;
Best Local Similarity 56.0%; Pred. No. 0.0014;
RESULT 799
ID ABV37264 standard; cDNA; 563 BP.
DE Human prostate expression marker cDNA 37255.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.1%; Score 49.6; DB 5; Length 563;
Best Local Similarity 54.8%; Pred. No. 0.0017;
RESULT 800
ID ABX78351 standard; cDNA; 932 BP.
DE Corn stress response protein EST #9.
PN US2002152497-A1.
PD 17-OCT-2002.
PA (FALC/) FALCO S C.
PA (FAMO/) FAMODU O O.
PA (MEYE/) MEYERS B C.
PA (MIAO/) MIAO G.
PA (ODEL/) ODELL J T.
PA (RAFA/) RAFALSKI J A.
PA (THOR/) THORPE C J.

PA (SAKA/) SAKAI H.
PA (WENG/) WENG Z.
Query Match 2.1%; Score 49.6; DB 10; Length 932;
Best Local Similarity 56.0%; Pred. No. 0.0024;
RESULT 801
ID AAT62123 standard; cDNA to mRNA; 1578 BP.
DE Solanum melongena flavanoid-3-glucosyl transferase cDNA.
PN JP09056385-A.
PD 04-MAR-1997.
PA (KIRI) KIRIN BREWERY KK.
Query Match 2.1%; Score 49.4; DB 2; Length 1578;
Best Local Similarity 58.5%; Pred. No. 0.0039;
RESULT 802
ID AAH42961 standard; DNA; 656 BP.
DE Nucleic acid differentially expressed in Appl-d Drosophila.
PN WO200153538-A2.
PD 26-JUL-2001.
PA (NEUR-) NEUROSCIENCES RES FOUND INC.
Query Match 2.1%; Score 49.2; DB 4; Length 656;
Best Local Similarity 47.4%; Pred. No. 0.0025;
RESULT 803
ID ABX96761 standard; cDNA; 656 BP.
DE D. melanogaster differentially expressed mRNA EST GH04745.
PN US2002174447-A1.
PD 21-NOV-2002.
PA (GREE/) GREENSPAN R J.
PA (EDEL/) EDELMAN G M.
Query Match 2.1%; Score 49.2; DB 8; Length 656;
Best Local Similarity 47.4%; Pred. No. 0.0025;
RESULT 804
ID AAS05504 standard; DNA; 657 BP.
DE Mammalian vestibular system geotactic behaviour modulator gene #104.
PN WO200140519-A2.
PD 07-JUN-2001.
PA (NEUR-) NEUROSCIENCES RES FOUND INC.
Query Match 2.1%; Score 49.2; DB 5; Length 657;
Best Local Similarity 47.4%; Pred. No. 0.0025;
RESULT 805
ID ABL28715 standard; DNA; 1530 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37618.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.1%; Score 49.2; DB 4; Length 1530;
Best Local Similarity 59.2%; Pred. No. 0.0043;
RESULT 806
ID ABL20759 standard; DNA; 1752 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 13750.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.1%; Score 49.2; DB 4; Length 1752;
Best Local Similarity 47.4%; Pred. No. 0.0048;
RESULT 807
ID ABL28714 standard; DNA; 3679 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37615.
PN WO200171042-A2.

PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.1%; Score 49.2; DB 4; Length 3679;
Best Local Similarity 59.2%; Pred. No. 0.0078;
RESULT 808
ID ABV07329 standard; cDNA; 501 BP.
DE Human prostate expression marker cDNA 7320.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.1%; Score 49; DB 5; Length 501;
Best Local Similarity 54.8%; Pred. No. 0.0024;
RESULT 809
ID ADJ12032 standard; DNA; 1052 BP.
DE Wheat cDNA modulated by post-transcriptional gene silencing SeqID 668.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
Query Match 2.1%; Score 49; DB 11; Length 1052;
Best Local Similarity 57.5%; Pred. No. 0.0039;
RESULT 810
ID ABQ60746 standard; cDNA; 558 BP.
DE Human colon cancer related nucleotide sequence SEQ ID NO:4441.
PN WO200229086-A2.
PD 11-APR-2002.
PA (FARB) BAYER CORP.
Query Match 2.1%; Score 48.8; DB 6; Length 558;
Best Local Similarity 46.2%; Pred. No. 0.0029;
RESULT 811
ID ADA49280 standard; DNA; 666 BP.
DE Maize gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.1%; Score 48.6; DB 9; Length 666;
Best Local Similarity 58.7%; Pred. No. 0.0038;
RESULT 812
ID AAH51513 standard; DNA; 1001 BP.
DE Human UGT2B10 related DNA containing a biallelic polymorphism SEQ ID 404.
PN WO200058508-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 2.1%; Score 48.6; DB 3; Length 1001;
Best Local Similarity 58.7%; Pred. No. 0.005;
RESULT 813
ID ADA71938 standard; DNA; 2000 BP.

DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.1%; Score 48.6; DB 8; Length 2000;
Best Local Similarity 12.4%; Pred. No. 0.0078;
RESULT 814
ID ADA49109 standard; DNA; 789 BP.
DE Wheat gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.1%; Score 48.4; DB 9; Length 789;
Best Local Similarity 57.1%; Pred. No. 0.0049;
RESULT 815
ID ABZ12395 standard; DNA; 1437 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 200.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.1%; Score 48.4; DB 6; Length 1437;
Best Local Similarity 55.2%; Pred. No. 0.0072;
RESULT 816
ID ADA71206 standard; DNA; 1455 BP.
DE Rice gene, SEQ ID 4529.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.1%; Score 48.4; DB 8; Length 1455;
Best Local Similarity 58.2%; Pred. No. 0.0073;
RESULT 817
ID AAX60622 standard; DNA; 2396 BP.
DE M. brassicae ecdysteroid UDP-glucosyl transferase DNA.
PN JP11123079-A.
PD 11-MAY-1999.
PA (NOYA-) NOYAKU BIOTECHNOLOGY KAIHATSU.
Query Match 2.1%; Score 48.4; DB 2; Length 2396;
Best Local Similarity 55.3%; Pred. No. 0.01;
RESULT 818
ID ADJ11847 standard; DNA; 551 BP.
DE Banana cDNA modulated by post-transcriptional gene silencing SeqID 483.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
Query Match 2.1%; Score 48.2; DB 11; Length 551;

Best Local Similarity 56.7%; Pred. No. 0.0044;
RESULT 819
ID ADJ43854 standard; cDNA; 551 BP.
DE Plant cDNA #4854.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 2.1%; Score 48.2; DB 12; Length 551;
Best Local Similarity 56.7%; Pred. No. 0.0044;
RESULT 820
ID ABX77212 standard; DNA; 75798 BP.
DE Mouse uridine diphosphoglucuronosyl transferase gene locus.
PN WO200283897-A1.
PD 24-OCT-2002.
PA (GENE-) GENE STREAM PTY LTD.
Query Match 2.1%; Score 48.2; DB 10; Length 75798;
Best Local Similarity 49.8%; Pred. No. 0.12;
RESULT 821
ID AAC39201 standard; DNA; 1689 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 23745.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.1%; Score 48; DB 3; Length 1689;
Best Local Similarity 56.2%; Pred. No. 0.011;
RESULT 822
ID ABK73606 standard; DNA; 1138 BP.
DE Bacillus licheniformis genomic sequence tag (GST) #897.
PN WO200229113-A2.
PD 11-APR-2002.
PA (NOVO) NOVOZYMES BIOTECH INC.
PA (NOVO) NOVOZYMES AS.
Query Match 2.1%; Score 47.8; DB 6; Length 1138;
Best Local Similarity 51.7%; Pred. No. 0.0094;
RESULT 823
ID ADA69896 standard; DNA; 1410 BP.
DE Rice gene, SEQ ID 3219.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.0%; Score 47.4; DB 8; Length 1410;
Best Local Similarity 55.2%; Pred. No. 0.014;
RESULT 824
ID ADA11031 standard; cDNA; 334 BP.
DE Human cDNA differentially expressed in colon cancer #104.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.

PA (JONE/) JONES D A.
Query Match 2.0%; Score 46.6; DB 9; Length 334;
Best Local Similarity 58.9%; Pred. No. 0.0095;
RESULT 825
ID AAD59156 standard; cDNA; 334 BP.
DE Human UDP-glucuronosyltransferase cDNA #1.
PN US2003073105-A1.
PD 17-APR-2003.
PA (LASE/) LASEK A K W.
PA (SORN/) SORNASSE T.
Query Match 2.0%; Score 46.6; DB 10; Length 334;
Best Local Similarity 58.9%; Pred. No. 0.0095;
RESULT 826
ID ADJ11840 standard; DNA; 634 BP.
DE Banana cDNA modulated by post-transcriptional gene silencing SeqID 476.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
Query Match 2.0%; Score 46.6; DB 11; Length 634;
Best Local Similarity 58.2%; Pred. No. 0.014;
RESULT 827
ID ABX40687 standard; cDNA; 315 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #5852.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.0%; Score 46.4; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 0.01;
RESULT 828
ID ACC62594 standard; cDNA; 542 BP.
DE Rice endosperm EST #13.
PN CN1366079-A.
PD 28-AUG-2002.
PA (UYZH-) UNIV ZHEJIANG.
Query Match 2.0%; Score 46.4; DB 8; Length 542;
Best Local Similarity 55.6%; Pred. No. 0.015;
RESULT 829
ID AAD13658 standard; DNA; 1440 BP.
DE Arabidopsis thaliana glucosyltransferase (GTase) A42 gene.
PN WO200159140-A1.
PD 16-AUG-2001.
PA (UYYO-) UNIV YORK.
Query Match 2.0%; Score 46.4; DB 4; Length 1440;

Best Local Similarity 55.6%; Pred. No. 0.029;
RESULT 830
ID ABZ12275 standard; DNA; 1440 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 80.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.0%; Score 46.4; DB 6; Length 1440;
Best Local Similarity 55.6%; Pred. No. 0.029;
RESULT 831
ID ADC25958 standard; DNA; 1440 BP.
DE Thale cress UDP-glucosyltransferase DNA 2.
PN WO2003066836-A2.
PD 14-AUG-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 2.0%; Score 46.4; DB 10; Length 1440;
Best Local Similarity 55.6%; Pred. No. 0.029;
RESULT 832
ID AAC47208 standard; DNA; 1688 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52959.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.0%; Score 46.4; DB 3; Length 1688;
Best Local Similarity 55.6%; Pred. No. 0.032;
RESULT 833
ID ADL14332 standard; DNA; 1751 BP.
DE DNA encoding a carnation glycosyltransferase enzyme SeqID 1.
PN WO2004018682-A1.
PD 04-MAR-2004.
PA (SUNR) SUNTORY LTD.
PA (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.
Query Match 2.0%; Score 46.4; DB 12; Length 1751;
Best Local Similarity 51.4%; Pred. No. 0.033;
RESULT 834
ID AAL23790 standard; cDNA; 490 BP.
DE Human breast cancer expressed polynucleotide 16247.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.0%; Score 46.2; DB 4; Length 490;
Best Local Similarity 59.5%; Pred. No. 0.016;
RESULT 835
ID ADK59883 standard; DNA; 631 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #7266.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 2.0%; Score 46.2; DB 10; Length 631;
Best Local Similarity 55.2%; Pred. No. 0.019;
RESULT 836
ID ADA70992 standard; DNA; 1458 BP.
DE Rice gene, SEQ ID 4315.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 2.0%; Score 46.2; DB 8; Length 1458;
Best Local Similarity 57.1%; Pred. No. 0.033;
RESULT 837
ID ADA70251 standard; DNA; 1464 BP.
DE Rice gene, SEQ ID 3574.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.0%; Score 46.2; DB 8; Length 1464;
Best Local Similarity 57.1%; Pred. No. 0.033;
RESULT 838
ID ABX34472 standard; cDNA; 1983 BP.
DE Human mddt cDNA SEQ ID 33.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.0%; Score 46.2; DB 8; Length 1983;
Best Local Similarity 53.6%; Pred. No. 0.041;
RESULT 839
ID ABL17597 standard; DNA; 1477 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4264.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.0%; Score 46; DB 4; Length 1477;
Best Local Similarity 44.7%; Pred. No. 0.038;
RESULT 840
ID ABL17596 standard; DNA; 3528 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4261.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.0%; Score 46; DB 4; Length 3528;
Best Local Similarity 44.7%; Pred. No. 0.068;
RESULT 841
ID ADA71335 standard; DNA; 1395 BP.
DE Rice gene, SEQ ID 4658.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.0%; Score 45.8; DB 8; Length 1395;
Best Local Similarity 57.2%; Pred. No. 0.042;
RESULT 842
ID ABL32281 standard; DNA; 13511 BP.
DE Human immune system associated gene SEQ ID NO: 254.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 45.8; DB 6; Length 13511;
Best Local Similarity 50.7%; Pred. No. 0.19;
RESULT 843
ID ABL34609 standard; DNA; 18585 BP.
DE Human metastasis associated gene SEQ ID NO: 162.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 45.8; DB 6; Length 18585;

Best Local Similarity 49.4%; Pred. No. 0.24;
RESULT 844
ID ADS99870 standard; DNA; 18585 BP.
DE Complement of bisulphite treated metastasis-associated human gene #81.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 2.0%; Score 45.8; DB 7; Length 18585;
Best Local Similarity 49.4%; Pred. No. 0.24;
RESULT 845
ID ADS65831 standard; cDNA; 242 BP.
DE Corn seedling-derived polynucleotide (cpds), SEQ ID 847.
PN US2003237110-A9.
PD 25-DEC-2003.
PA (INCY-) INCYTE PHARM INC.
Query Match 1.9%; Score 45.2; DB 7; Length 242;
Best Local Similarity 59.2%; Pred. No. 0.02;
RESULT 846
ID ADA69839 standard; DNA; 1383 BP.
DE Rice gene, SEQ ID 3162.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.9%; Score 45.2; DB 8; Length 1383;
Best Local Similarity 55.8%; Pred. No. 0.064;
RESULT 847
ID ADA70476 standard; DNA; 1452 BP.
DE Rice gene, SEQ ID 3799.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.9%; Score 45.2; DB 8; Length 1452;
Best Local Similarity 55.8%; Pred. No. 0.066;
RESULT 848
ID ADA48529 standard; DNA; 1549 BP.
DE Rice gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.9%; Score 45.2; DB 9; Length 1549;
Best Local Similarity 55.8%; Pred. No. 0.069;
RESULT 849
ID ABX78358 standard; cDNA; 1736 BP.
DE Wheat stress response protein cDNA #2.
PN US2002152497-A1.
PD 17-OCT-2002.
PA (FALC/) FALCO S C.
PA (FAMO/) FAMODU O O.
PA (MEYE/) MEYERS B C.
PA (MIAO/) MIAO G.
PA (ODEL/) ODELL J T.
PA (RAFA/) RAFALSKI J A.
PA (THOR/) THORPE C J.
PA (SAKA/) SAKAI H.
PA (WENG/) WENG Z.

Query Match 1.9%; Score 45.2; DB 10; Length 1736;
Best Local Similarity 55.8%; Pred. No. 0.074;
RESULT 850
ID ADA72551 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5876.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.9%; Score 45.2; DB 8; Length 2000;
Best Local Similarity 55.8%; Pred. No. 0.081;
RESULT 851
ID AAC58024 standard; DNA; 45 BP.
DE Human PRO1780 hybridisation probe SEQ ID NO:16.
PN WO200053750-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 3; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 852
ID AAA37270 standard; DNA; 45 BP.
DE Human PRO1780 hybridisation probe SEQ ID NO:285.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 3; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 853
ID AAF54404 standard; DNA; 45 BP.
DE Primer #83 used in the identification of proteins.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 854
ID ACD68443 standard; DNA; 45 BP.
DE Novel human secreted and transmembrane protein related probe #41.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 855
ID ACH04545 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 856
ID ACD68089 standard; DNA; 45 BP.
DE Novel human secreted and transmembrane protein related probe #41.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 9; Length 45;

Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 857
ID ADC18154 standard; DNA; 45 BP.
DE Human PRO probe #41.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 858
ID ADD70800 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 859
ID ADD39877 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 860
ID ADD70323 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 861
ID ADD38444 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 862
ID ADD39400 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 863
ID ADD38923 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 864

ID ADD40354 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 865

ID ADE50575 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 866

ID ADE20187 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 867

ID ADE50098 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 868

ID ADE21656 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 869

ID ADF30081 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 870

ID ADF55974 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 871

ID ADH99478 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 872

ID ADE96658 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 873

ID ADF25969 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 874

ID ADF24868 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 875

ID ADF29604 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 876

ID ADE97135 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 877

ID ADH03173 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 878

ID ADH04127 standard; DNA; 45 BP.

DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 879
ID ADH03650 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 880
ID ADH04604 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 881
ID ADH61605 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 882
ID ADL94804 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 883
ID ADC25977 standard; DNA; 1515 BP.
DE Calamondin plant UDP-glucosyltransferase DNA.
PN WO2003066836-A2.
PD 14-AUG-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.9%; Score 45; DB 10; Length 1515;
Best Local Similarity 56.4%; Pred. No. 0.078;
RESULT 884
ID AAI71192 standard; cDNA; 1536 BP.
DE Citrus unshiu UDP-D glucose:limonoid glucosyltransferase cDNA SEQ:10.
PN JP2001204477-A.
PD 31-JUL-2001.
PA (NORQ) NORINSUISANSHO KAJU SHIKENBACHO.
Query Match 1.9%; Score 45; DB 4; Length 1536;
Best Local Similarity 56.4%; Pred. No. 0.078;
RESULT 885
ID ADC25980 standard; DNA; 1560 BP.
DE Calamondin plant UDP-glucosyltransferase DNA variant.

PN WO2003066836-A2.
PD 14-AUG-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.9%; Score 45; DB 10; Length 1560;
Best Local Similarity 56.4%; Pred. No. 0.079;
RESULT 886
ID AAI71187 standard; cDNA; 1732 BP.
DE Citrus unshiu UDP-D glucose:limonoid glucosyltransferase cDNA SEQ:1.
PN JP2001204477-A.
PD 31-JUL-2001.
PA (NORQ) NORINSUISANSHO KAJU SHIKENBACHO.
Query Match 1.9%; Score 45; DB 4; Length 1732;
Best Local Similarity 56.4%; Pred. No. 0.085;
RESULT 887
ID AAI96011 standard; cDNA; 774 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 2086.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 1.9%; Score 44.8; DB 4; Length 774;
Best Local Similarity 55.9%; Pred. No. 0.057;
RESULT 888
ID AAC43085 standard; DNA; 1362 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 37972.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.9%; Score 44.8; DB 3; Length 1362;
Best Local Similarity 55.0%; Pred. No. 0.083;
RESULT 889
ID ABZ14612 standard; DNA; 1362 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2417.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.9%; Score 44.8; DB 6; Length 1362;
Best Local Similarity 55.0%; Pred. No. 0.083;
RESULT 890
ID ADG87939 standard; cDNA; 1362 BP.
DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #381.
PN WO200222675-A2.
PD 21-MAR-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (UYNC-) UNIV NORTH CAROLINA.
PA (GLAZ/) GLAZEBROOK J.
PA (WANG/) WANG X.
PA (DANG/) DANGL J L.
PA (EULG/) EULGEM T.
PA (ZHUT/) ZHU T.
Query Match 1.9%; Score 44.8; DB 6; Length 1362;
Best Local Similarity 55.0%; Pred. No. 0.083;
RESULT 891
ID ABZ42019 standard; cDNA; 1362 BP.
DE Arabidopsis thaliana gene #3 modulated by PTGS.
PN WO200281695-A2.
PD 17-OCT-2002.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (FRIE-) FRIEDRICH MIESCHER INST.
Query Match 1.9%; Score 44.8; DB 8; Length 1362;
Best Local Similarity 55.0%; Pred. No. 0.083;
RESULT 892
ID ADA68251 standard; DNA; 1362 BP.
DE Arabidopsis thaliana gene, SEQ ID 899.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.9%; Score 44.8; DB 8; Length 1362;
Best Local Similarity 55.0%; Pred. No. 0.083;
RESULT 893
ID AAA68125 standard; DNA; 762 BP.
DE Pinus radiata flavonol glucosyl transferase DNA sequence SEQ ID NO:218.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 1.9%; Score 44.6; DB 3; Length 762;
Best Local Similarity 57.6%; Pred. No. 0.065;
RESULT 894
ID ADD41875 standard; DNA; 762 BP.
DE Flavonol glucosyl transferase DNA.
PN US2003131373-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Query Match 1.9%; Score 44.6; DB 10; Length 762;
Best Local Similarity 57.6%; Pred. No. 0.065;
RESULT 895
ID ADC25964 standard; cDNA; 1437 BP.
DE Grape UDP-glucosyltransferase cDNA.
PN WO2003066836-A2.
PD 14-AUG-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.9%; Score 44.6; DB 10; Length 1437;
Best Local Similarity 55.5%; Pred. No. 0.099;
RESULT 896
ID AAT68693 standard; cDNA; 432 BP.
DE Strawberry UDP-glucuronosyl transferase cDNA.
PN WO9721816-A1.
PD 19-JUN-1997.
PA (ZENE) ZENECA LTD.
Query Match 1.9%; Score 43.8; DB 2; Length 432;
Best Local Similarity 56.6%; Pred. No. 0.077;
RESULT 897
ID ADA70053 standard; DNA; 1152 BP.
DE Rice gene, SEQ ID 3376.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.9%; Score 43.8; DB 8; Length 1152;
Best Local Similarity 56.6%; Pred. No. 0.15;
RESULT 898
ID ADJ11565 standard; DNA; 1152 BP.
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 201.

PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
Query Match 1.9%; Score 43.8; DB 11; Length 1152;
Best Local Similarity 56.6%; Pred. No. 0.15;
RESULT 899
ID ADA69724 standard; DNA; 1482 BP.
DE Rice gene, SEQ ID 3047.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.9%; Score 43.8; DB 8; Length 1482;
Best Local Similarity 54.7%; Pred. No. 0.17;
RESULT 900
ID AAI61373 standard; DNA; 513445 BP.
DE Soybean 318013 region A3, SEQ ID NO: 4.
PN WO200151627-A2.
PD 19-JUL-2001.
PA (MONS) MONSANTO CO.
Query Match 1.9%; Score 43.8; DB 5; Length 110000;
Best Local Similarity 53.1%; Pred. No. 3;
RESULT 901
ID AAH51524 standard; DNA; 1001 BP.
DE Human UGT2B15 related DNA containing a biallelic polymorphism SEQ ID 415.
PN WO200058508-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 1.9%; Score 43.6; DB 3; Length 1001;
Best Local Similarity 56.2%; Pred. No. 0.15;
RESULT 902
ID AAH51522 standard; DNA; 1001 BP.
DE Human UGT2B15 related DNA containing a biallelic polymorphism SEQ ID 413.
PN WO200058508-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 1.9%; Score 43.6; DB 3; Length 1001;
Best Local Similarity 56.2%; Pred. No. 0.15;
RESULT 903
ID AAH51523 standard; DNA; 1001 BP.
DE Human UGT2B15 related DNA containing a biallelic polymorphism SEQ ID 414.
PN WO200058508-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 1.9%; Score 43.6; DB 3; Length 1001;
Best Local Similarity 56.2%; Pred. No. 0.15;
RESULT 904

ID AAH51526 standard; DNA; 1001 BP.
DE Human UGT2B15 related DNA containing a biallelic polymorphism SEQ ID 417.
PN WO200058508-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
 Query Match 1.9%; Score 43.6; DB 3; Length 1001;
 Best Local Similarity 56.2%; Pred. No. 0.15;
RESULT 905
ID AAZ95208 standard; DNA; 1020 BP.
DE Human UGT2B15 exon 2 nucleotide sequence.
PN WO200006776-A1.
PD 10-FEB-2000.
PA (AXYS-) AXYS PHARM INC.
 Query Match 1.9%; Score 43.6; DB 3; Length 1020;
 Best Local Similarity 56.2%; Pred. No. 0.16;
RESULT 906
ID ABZ13997 standard; DNA; 1350 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1802.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.9%; Score 43.6; DB 6; Length 1350;
 Best Local Similarity 56.2%; Pred. No. 0.19;
RESULT 907
ID ADG87992 standard; cDNA; 1350 BP.
DE A. thaliana RPP4-upregulated pathogen infection-related gene #434.
PN WO200222675-A2.
PD 21-MAR-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (UYNC-) UNIV NORTH CAROLINA.
PA (GLAZ/) GLAZEBROOK J.
PA (WANG/) WANG X.
PA (DANG/) DANGL J L.
PA (EULG/) EULGEM T.
PA (ZHUT/) ZHU T.
 Query Match 1.9%; Score 43.6; DB 6; Length 1350;
 Best Local Similarity 56.2%; Pred. No. 0.19;
RESULT 908
ID ADA68085 standard; DNA; 1350 BP.
DE Arabidopsis thaliana gene, SEQ ID 345.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.9%; Score 43.6; DB 8; Length 1350;
 Best Local Similarity 56.2%; Pred. No. 0.19;
RESULT 909
ID AAD13679 standard; DNA; 1437 BP.
DE Arabidopsis thaliana glucosyltransferase (GTase) UGT74F2 DNA.
PN WO200159140-A1.
PD 16-AUG-2001.
PA (UYYO-) UNIV YORK.
 Query Match 1.9%; Score 43.6; DB 4; Length 1437;
 Best Local Similarity 56.2%; Pred. No. 0.2;
RESULT 910
ID ADJ83915 standard; DNA; 1437 BP.
DE Thale cress glucosyltransferase 74F2 ORF DNA.

PN WO2003106688-A1.
PD 24-DEC-2003.
PA (UYYO-) UNIV YORK.
Query Match 1.9%; Score 43.6; DB 12; Length 1437;
Best Local Similarity 56.2%; Pred. No. 0.2;
RESULT 911
ID AAC42649 standard; DNA; 1527 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36344.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.9%; Score 43.6; DB 3; Length 1527;
Best Local Similarity 56.2%; Pred. No. 0.2;
RESULT 912
ID AAC37656 standard; DNA; 1565 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 18186.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.9%; Score 43.6; DB 3; Length 1565;
Best Local Similarity 53.5%; Pred. No. 0.21;
RESULT 913
ID ADJ44409 standard; cDNA; 678 BP.
DE Plant cDNA #5409.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 1.9%; Score 43.4; DB 12; Length 678;
Best Local Similarity 56.7%; Pred. No. 0.14;
RESULT 914
ID ADA71177 standard; DNA; 1359 BP.
DE Rice gene, SEQ ID 4500.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.9%; Score 43.4; DB 8; Length 1359;
Best Local Similarity 54.1%; Pred. No. 0.22;
RESULT 915
ID AAH51525 standard; DNA; 1001 BP.
DE Human UGT2B15 related DNA containing a biallelic polymorphism SEQ ID 416.
PN WO200058508-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 1.9%; Score 43.2; DB 3; Length 1001;
Best Local Similarity 55.5%; Pred. No. 0.2;
RESULT 916
ID ABL34122 standard; DNA; 10329 BP.
DE Human immune system associated gene SEQ ID NO: 2095.
PN WO200200928-A2.

PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 43.2; DB 6; Length 10329;
Best Local Similarity 50.0%; Pred. No. 0.96;
RESULT 917
ID ADA49272 standard; DNA; 393 BP.
DE Maize gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.9%; Score 43; DB 9; Length 393;
Best Local Similarity 54.0%; Pred. No. 0.13;
RESULT 918
ID ADJ44737 standard; cDNA; 393 BP.
DE Plant cDNA #5737.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 1.9%; Score 43; DB 12; Length 393;
Best Local Similarity 54.0%; Pred. No. 0.13;
RESULT 919
ID ADJ83914 standard; DNA; 1350 BP.
DE Thale cress glucosyltransferase 74F1 ORF DNA.
PN WO2003106688-A1.
PD 24-DEC-2003.
PA (UYYO-) UNIV YORK.
Query Match 1.9%; Score 43; DB 12; Length 1350;
Best Local Similarity 56.8%; Pred. No. 0.28;
RESULT 920
ID AAA54024 standard; DNA; 1440 BP.
DE Glucosyltransferase coding sequence.
PN WO200055340-A1.
PD 21-SEP-2000.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 1.9%; Score 43; DB 3; Length 1440;
Best Local Similarity 52.5%; Pred. No. 0.3;
RESULT 921
ID ADK59884 standard; DNA; 557 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #7267.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 1.8%; Score 42.8; DB 10; Length 557;
Best Local Similarity 55.3%; Pred. No. 0.18;
RESULT 922
ID ADA70052 standard; DNA; 1476 BP.

DE Rice gene, SEQ ID 3375.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 42.8; DB 8; Length 1476;
Best Local Similarity 55.3%; Pred. No. 0.35;
RESULT 923
ID AAA87154 standard; DNA; 164 BP.
DE Rat hepatocyte carcinogenesis biomarker nucleic acid SEQ ID NO:78.
PN WO200044902-A2.
PD 03-AUG-2000.
PA (SEAR) SEARLE & CO G D.
Query Match 1.8%; Score 42.6; DB 3; Length 164;
Best Local Similarity 68.7%; Pred. No. 0.092;
RESULT 924
ID ACC49462 standard; cDNA; 1368 BP.
DE Arabidopsis glucosyltransferase 75B2 nucleic acid sequence.
PN WO2003023035-A2.
PD 20-MAR-2003.
PA (UYYO-) UNIV YORK.
Query Match 1.8%; Score 42.6; DB 8; Length 1368;
Best Local Similarity 51.3%; Pred. No. 0.38;
RESULT 925
ID AAV29492 standard; cDNA to mRNA; 2025 BP.
DE DNA encoding ecdysteroid UDP-glycosyl transferase.
PN WO9814578-A1.
PD 09-APR-1998.
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
PA (AMCY) AMERICAN CYANAMID CO.
Query Match 1.8%; Score 42.6; DB 2; Length 2025;
Best Local Similarity 51.9%; Pred. No. 0.49;
RESULT 926
ID AAD07242 standard; DNA; 2025 BP.
DE HzSNPV ecdysteroid UDP-glucosyltransferase (egt) gene.
PN US6235278-B1.
PD 22-MAY-2001.
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
PA (AMCY) AMERICAN CYANAMID CO.
Query Match 1.8%; Score 42.6; DB 5; Length 2025;
Best Local Similarity 51.9%; Pred. No. 0.49;
RESULT 927
ID ABA81171 standard; DNA; 121 BP.
DE UGT1 mutation correcting oligonucleotide SEQ ID NO: 4017.
PN WO200173002-A2.
PD 04-OCT-2001.
PA (UYDE) UNIV DELAWARE.
Query Match 1.8%; Score 42.4; DB 4; Length 121;
Best Local Similarity 60.3%; Pred. No. 0.087;
RESULT 928
ID ABA81170 standard; DNA; 121 BP.
DE UGT1 mutation correcting oligonucleotide SEQ ID NO: 4016.
PN WO200173002-A2.
PD 04-OCT-2001.
PA (UYDE) UNIV DELAWARE.
Query Match 1.8%; Score 42.4; DB 4; Length 121;
Best Local Similarity 60.3%; Pred. No. 0.087;
RESULT 929

ID ABX47099 standard; cDNA; 234 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12264.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.8%; Score 42.4; DB 8; Length 234;
Best Local Similarity 57.6%; Pred. No. 0.13;
RESULT 930
ID ADK56213 standard; DNA; 372 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #3596.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 1.8%; Score 42.4; DB 10; Length 372;
Best Local Similarity 56.4%; Pred. No. 0.18;
RESULT 931
ID AAD13655 standard; DNA; 1410 BP.
DE Arabidopsis thaliana glucosyltransferase (GTase) A062 gene.
PN WO200159140-A1.
PD 16-AUG-2001.
PA (UYYO-) UNIV YORK.
Query Match 1.8%; Score 42.4; DB 4; Length 1410;
Best Local Similarity 51.6%; Pred. No. 0.44;
RESULT 932
ID ACC49461 standard; cDNA; 1410 BP.
DE Arabidopsis glucosyltransferase 75B1 nucleic acid sequence.
PN WO2003023035-A2.
PD 20-MAR-2003.
PA (UYYO-) UNIV YORK.
Query Match 1.8%; Score 42.4; DB 8; Length 1410;
Best Local Similarity 51.6%; Pred. No. 0.44;
RESULT 933
ID ABZ80609 standard; DNA; 1410 BP.
DE Arabidopsis thaliana glucosyltransferase clone 75B1.
PN WO2002103022-A2.
PD 27-DEC-2002.
PA (UYYO-) UNIV YORK.
Query Match 1.8%; Score 42.4; DB 8; Length 1410;
Best Local Similarity 51.6%; Pred. No. 0.44;
RESULT 934
ID ABZ14576 standard; DNA; 1428 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2381.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 1428;
Best Local Similarity 52.2%; Pred. No. 0.45;
RESULT 935
ID ADC25962 standard; DNA; 1428 BP.
DE Thale cress UDP-glucosyltransferase DNA 3.
PN WO2003066836-A2.
PD 14-AUG-2003.

PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.8%; Score 42.4; DB 10; Length 1428;
Best Local Similarity 52.2%; Pred. No. 0.45;
RESULT 936
ID AAD13659 standard; DNA; 1430 BP.
DE Arabidopsis thaliana glucosyltransferase (GTase) A43 gene.
PN WO200159140-A1.
PD 16-AUG-2001.
PA (UYYO-) UNIV YORK.
Query Match 1.8%; Score 42.4; DB 4; Length 1430;
Best Local Similarity 52.2%; Pred. No. 0.45;
RESULT 937
ID AAC47235 standard; DNA; 1533 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 53061.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 42.4; DB 3; Length 1533;
Best Local Similarity 52.2%; Pred. No. 0.47;
RESULT 938
ID AAC43061 standard; DNA; 1560 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 37881.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 42.4; DB 3; Length 1560;
Best Local Similarity 51.6%; Pred. No. 0.47;
RESULT 939
ID ADG88168 standard; cDNA; 1560 BP.
DE A. thaliana RPP4-upregulated pathogen infection-related gene #610.
PN WO200222675-A2.
PD 21-MAR-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (UYNC-) UNIV NORTH CAROLINA.
PA (GLAZ/) GLAZEBROOK J.
PA (WANG/) WANG X.
PA (DANG/) DANGL J L.
PA (EULG/) EULGEM T.
PA (ZHUT/) ZHU T.
Query Match 1.8%; Score 42.4; DB 6; Length 1560;
Best Local Similarity 51.6%; Pred. No. 0.47;
RESULT 940
ID ADA70893 standard; DNA; 1563 BP.
DE Rice gene, SEQ ID 4216.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 42.4; DB 8; Length 1563;
Best Local Similarity 55.4%; Pred. No. 0.47;
RESULT 941
ID AAC50249 standard; DNA; 1779 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 64128.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 42.4; DB 3; Length 1779;
Best Local Similarity 51.6%; Pred. No. 0.52;
RESULT 942
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.

PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 42.4; DB 8; Length 2000;
Best Local Similarity 8.7%; Pred. No. 0.56;
RESULT 943
Query Match 1.8%; Score 42.4; DB 5; Length 110000;
Best Local Similarity 52.9%; Pred. No. 8;
RESULT 944
ID ABN85750 standard; DNA; 180557 BP.
DE Human BAC clone RP11-334G22 SEQ ID NO 6.
PN US2002119929-A1.
PD 29-AUG-2002.
PA (BISH/) BISHOP C E.
PA (AGOU/) AGOULNIK A I.
PA (ZHUQ/) ZHU Q.
Query Match 1.8%; Score 42.4; DB 6; Length 180557;
Best Local Similarity 48.0%; Pred. No. 11;
RESULT 945
ID ABL34073 standard; DNA; 40862 BP.
DE Human immune system associated gene SEQ ID NO: 2046.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 40862;
Best Local Similarity 49.8%; Pred. No. 4.7;
RESULT 946
ID AAC40101 standard; DNA; 1525 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 27052.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 42; DB 3; Length 1525;
Best Local Similarity 51.7%; Pred. No. 0.61;
RESULT 947
ID AAQ10336 standard; DNA; 1800 BP.
DE Ecdysteroid UDP-glucosyl transferase gene.
PN WO9100014-A.
PD 10-JAN-1991.
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
Query Match 1.8%; Score 42; DB 2; Length 1800;
Best Local Similarity 51.0%; Pred. No. 0.68;
RESULT 948
ID AAT17233 standard; DNA; 2793 BP.
DE AcMNPV L-1 egt gene region.
PN WO9603509-A2.
PD 08-FEB-1996.
PA (AMCY) AMERICAN CYANAMID CO.
Query Match 1.8%; Score 42; DB 2; Length 2793;
Best Local Similarity 51.0%; Pred. No. 0.92;
RESULT 949
ID AAF23741 standard; DNA; 2793 BP.
DE egt coding sequence.
PN US6156309-A.
PD 05-DEC-2000.
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
PA (AMCY) AMERICAN CYANAMID CO.

Query Match 1.8%; Score 42; DB 4; Length 2793;
Best Local Similarity 51.0%; Pred. No. 0.92;
RESULT 950
ID ABQ67150 standard; DNA; 40324 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 180.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 40324;
Best Local Similarity 47.1%; Pred. No. 5.4;
RESULT 951
ID ADC51644 standard; DNA; 50000 BP.
DE BmNPV genomic DNA nucleotides 1-50000.
PN JP2003024062-A.
PD 28-JAN-2003.
PA (RIKA) RIKAGAKU KENKYUSHO.
Query Match 1.8%; Score 42; DB 10; Length 50000;
Best Local Similarity 51.0%; Pred. No. 6.2;
RESULT 952
ID AAT13635 standard; DNA; 133894 BP.
DE AcNPV genomic DNA clone 6.
PN WO9601320-A2.
PD 18-JAN-1996.
PA (NATU-) NATURAL ENVIRONMENT RES COUNCIL.
Query Match 1.8%; Score 42; DB 2; Length 133894;
Best Local Similarity 51.0%; Pred. No. 12;
RESULT 953
ID ADN98817 standard; cDNA; 957 BP.
DE Novel human cDNA sequence #417.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 1.8%; Score 41.8; DB 12; Length 957;
Best Local Similarity 50.2%; Pred. No. 0.52;
RESULT 954
ID ADO00386 standard; cDNA; 957 BP.
DE Novel human cDNA sequence #1201.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 1.8%; Score 41.8; DB 12; Length 957;
Best Local Similarity 50.2%; Pred. No. 0.52;
RESULT 955
ID ADN97656 standard; DNA; 1218 BP.
DE S ambofaciens spiramycin biosynthetic gene ORF26.
PN WO2004033689-A2.
PD 22-APR-2004.
PA (AVET) AVENTIS PHARMA SA.
PA (CNRS) CNRS.
Query Match 1.8%; Score 41.8; DB 12; Length 1218;
Best Local Similarity 50.8%; Pred. No. 0.61;
RESULT 956
ID AAC51291 standard; DNA; 1470 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 67973.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 41.8; DB 3; Length 1470;

Best Local Similarity 57.1%; Pred. No. 0.69;
RESULT 957
ID ADN73090 standard; cDNA; 1470 BP.
DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 985.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 1.8%; Score 41.8; DB 12; Length 1470;
Best Local Similarity 57.1%; Pred. No. 0.69;
RESULT 958
ID AAX02828 standard; cDNA; 2062 BP.
DE WO9905287 Seq ID 3.
PN WO9905287-A1.
PD 04-FEB-1999.
PA (SUNR) SUNTORY LTD.
Query Match 1.8%; Score 41.8; DB 2; Length 2062;
Best Local Similarity 50.2%; Pred. No. 0.86;
RESULT 959
ID ADN97683 standard; DNA; 6174 BP.
DE S ambofaciens spiramycin biosynthetic gene related sequence.
PN WO2004033689-A2.
PD 22-APR-2004.
PA (AVET) AVENTIS PHARMA SA.
PA (CNRS) CNRS.
Query Match 1.8%; Score 41.8; DB 12; Length 6174;
Best Local Similarity 50.8%; Pred. No. 1.8;
RESULT 960
ID ADN97655 standard; DNA; 10325 BP.
DE S ambofaciens spiramycin biosynthetic gene related sequence.
PN WO2004033689-A2.
PD 22-APR-2004.
PA (AVET) AVENTIS PHARMA SA.
PA (CNRS) CNRS.
Query Match 1.8%; Score 41.8; DB 12; Length 10325;
Best Local Similarity 50.8%; Pred. No. 2.5;
RESULT 961
ID ADN97689 standard; DNA; 12134 BP.
DE S ambofaciens spiramycin biosynthetic gene related sequence.
PN WO2004033689-A2.
PD 22-APR-2004.
PA (AVET) AVENTIS PHARMA SA.
PA (CNRS) CNRS.
Query Match 1.8%; Score 41.8; DB 12; Length 12134;
Best Local Similarity 50.8%; Pred. No. 2.8;
RESULT 962
ID ADA70300 standard; DNA; 1323 BP.
DE Rice gene, SEQ ID 3623.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 41.6; DB 8; Length 1323;
Best Local Similarity 55.6%; Pred. No. 0.73;
RESULT 963
ID ABL32448 standard; DNA; 7238 BP.
DE Human immune system associated gene SEQ ID NO: 421.
PN WO200200928-A2.
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 7238;
Best Local Similarity 49.5%; Pred. No. 2.3;
RESULT 964
ID AAD13683 standard; DNA; 1434 BP.
DE Arabidopsis thaliana glucosyltransferase (GTase) UGT76E2 DNA.
PN WO200159140-A1.
PD 16-AUG-2001.
PA (UYYO-) UNIV YORK.
Query Match 1.8%; Score 41.4; DB 4; Length 1434;
Best Local Similarity 53.4%; Pred. No. 0.89;
RESULT 965
ID AAC36320 standard; DNA; 1507 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 13360.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 41.4; DB 3; Length 1507;
Best Local Similarity 53.4%; Pred. No. 0.92;
RESULT 966
ID ABZ13771 standard; DNA; 1374 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1576.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 41.2; DB 6; Length 1374;
Best Local Similarity 55.6%; Pred. No. 0.99;
RESULT 967
ID ADA68399 standard; DNA; 1374 BP.
DE Arabidopsis thaliana gene, SEQ ID 718.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 41.2; DB 8; Length 1374;
Best Local Similarity 55.6%; Pred. No. 0.99;
RESULT 968
ID ADN73930 standard; cDNA; 1374 BP.
DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 1825.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 1.8%; Score 41.2; DB 12; Length 1374;
Best Local Similarity 55.6%; Pred. No. 0.99;
RESULT 969
ID ADA71282 standard; DNA; 4686 BP.
DE Rice gene, SEQ ID 4605.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 41.2; DB 8; Length 4686;
Best Local Similarity 57.9%; Pred. No. 2.2;
RESULT 970
ID ABL33105 standard; DNA; 7829 BP.
DE Human immune system associated gene SEQ ID NO: 1078.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.8%; Score 41.2; DB 6; Length 7829;
Best Local Similarity 49.5%; Pred. No. 3.1;
RESULT 971
ID ABK31287 standard; DNA; 7829 BP.
DE Signal transduction associated gene modified complementary DNA #65.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.2; DB 6; Length 7829;
Best Local Similarity 49.5%; Pred. No. 3.1;
RESULT 972
ID ABL70266 standard; DNA; 7829 BP.
DE Chemically treated cell signalling DNA sequence complementary to#78.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.2; DB 6; Length 7829;
Best Local Similarity 49.5%; Pred. No. 3.1;
RESULT 973
ID AAS61191 standard; DNA; 7829 BP.
DE Human gene regulation-associated gene oligonucleotide #146.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.2; DB 6; Length 7829;
Best Local Similarity 49.5%; Pred. No. 3.1;
RESULT 974
ID ABL32893 standard; DNA; 10710 BP.
DE Human immune system associated gene SEQ ID NO: 866.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.2; DB 6; Length 10710;
Best Local Similarity 49.5%; Pred. No. 3.9;
RESULT 975
ID ADJ39974 standard; cDNA; 485 BP.
DE Plant cDNA #974.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 1.8%; Score 41; DB 12; Length 485;
Best Local Similarity 55.2%; Pred. No. 0.57;
RESULT 976
ID ADA70477 standard; DNA; 1479 BP.
DE Rice gene, SEQ ID 3800.
PN WO2003000898-A1.
PD 03-JAN-2003.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 41; DB 8; Length 1479;
Best Local Similarity 55.2%; Pred. No. 1.2;
RESULT 977
ID ADA72552 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5877.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 41; DB 8; Length 2000;
Best Local Similarity 55.2%; Pred. No. 1.5;
RESULT 978
ID ACN45034 standard; DNA; 99588 BP.
DE Human genomic sequence hCG1640838.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.8%; Score 41; DB 11; Length 99588;
Best Local Similarity 50.8%; Pred. No. 20;
RESULT 979
ID AAA87085 standard; DNA; 366 BP.
DE Rat hepatocyte carcinogenesis biomarker nucleic acid SEQ ID NO:6.
PN WO200044902-A2.
PD 03-AUG-2000.
PA (SEAR) SEARLE & CO G D.
Query Match 1.8%; Score 40.8; DB 3; Length 366;
Best Local Similarity 50.8%; Pred. No. 0.54;
RESULT 980
ID ACN57109 standard; cDNA; 623 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-014-Q6-K6-D3, SEQ:11890.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.8%; Score 40.8; DB 13; Length 623;
Best Local Similarity 55.7%; Pred. No. 0.77;
RESULT 981
ID ADA69887 standard; DNA; 1398 BP.
DE Rice gene, SEQ ID 3210.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 40.8; DB 8; Length 1398;
Best Local Similarity 55.7%; Pred. No. 1.3;
RESULT 982
Query Match 1.8%; Score 40.8; DB 6; Length 110000;
Best Local Similarity 50.0%; Pred. No. 24;
RESULT 983
Query Match 1.8%; Score 40.8; DB 12; Length 110000;
Best Local Similarity 50.0%; Pred. No. 24;
RESULT 984
Query Match 1.8%; Score 40.8; DB 12; Length 110000;
Best Local Similarity 50.0%; Pred. No. 24;
RESULT 985
Query Match 1.8%; Score 40.8; DB 12; Length 110000;

Best Local Similarity 50.0%; Pred. No. 24;
RESULT 986
ID ABX43759 standard; cDNA; 427 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #8924.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.7%; Score 40.4; DB 8; Length 427;
Best Local Similarity 50.0%; Pred. No. 0.79;
RESULT 987
ID ADA69472 standard; DNA; 1437 BP.
DE Rice gene, SEQ ID 2795.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.7%; Score 40.4; DB 8; Length 1437;
Best Local Similarity 54.8%; Pred. No. 1.8;
RESULT 988
ID ACC49459 standard; cDNA; 1440 BP.
DE Arabidopsis glucosyltransferase 71B6 nucleic acid sequence.
PN WO2003023035-A2.
PD 20-MAR-2003.
PA (UYYO-) UNIV YORK.
Query Match 1.7%; Score 40.4; DB 8; Length 1440;
Best Local Similarity 52.3%; Pred. No. 1.8;
RESULT 989
ID ADJ11934 standard; DNA; 468 BP.
DE Wheat cDNA modulated by post-transcriptional gene silencing SeqID 570.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
Query Match 1.7%; Score 40.2; DB 11; Length 468;
Best Local Similarity 55.3%; Pred. No. 0.96;
RESULT 990
ID ADN74714 standard; cDNA; 1383 BP.
DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 2609.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 1.7%; Score 40.2; DB 12; Length 1383;
Best Local Similarity 54.4%; Pred. No. 2;
RESULT 991
ID ADR70667 standard; cDNA; 1613 BP.

DE Solanum aculeatissimum glycosylase encoding cDNA SEQ ID NO:4.
PN WO2004078979-A1.
PD 16-SEP-2004.
PA (RIKE) RIKEN KK.
Query Match 1.7%; Score 40.2; DB 13; Length 1613;
Best Local Similarity 50.8%; Pred. No. 2.2;
RESULT 992
ID ADR70665 standard; cDNA; 1673 BP.
DE Solanum aculeatissimum glycosylase encoding cDNA SEQ ID NO:2.
PN WO2004078979-A1.
PD 16-SEP-2004.
PA (RIKE) RIKEN KK.
Query Match 1.7%; Score 40.2; DB 13; Length 1673;
Best Local Similarity 50.8%; Pred. No. 2.2;
RESULT 993
ID ADA70478 standard; DNA; 1350 BP.
DE Rice gene, SEQ ID 3801.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.7%; Score 40; DB 8; Length 1350;
Best Local Similarity 53.2%; Pred. No. 2.2;
RESULT 994
ID AAC51614 standard; DNA; 1362 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 69162.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.7%; Score 40; DB 3; Length 1362;
Best Local Similarity 53.9%; Pred. No. 2.2;
RESULT 995
ID AAD13682 standard; DNA; 1457 BP.
DE Arabidopsis thaliana glucosyltransferase (GTase) UGT76E12 DNA.
PN WO200159140-A1.
PD 16-AUG-2001.
PA (UYYO-) UNIV YORK.
Query Match 1.7%; Score 40; DB 4; Length 1457;
Best Local Similarity 53.9%; Pred. No. 2.4;
RESULT 996
ID ABL33993 standard; DNA; 6029 BP.
DE Human immune system associated gene SEQ ID NO: 1966.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 40; DB 6; Length 6029;
Best Local Similarity 49.1%; Pred. No. 6;
RESULT 997
ID ABL32860 standard; DNA; 7631 BP.
DE Human immune system associated gene SEQ ID NO: 833.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 40; DB 6; Length 7631;
Best Local Similarity 53.9%; Pred. No. 7.1;
RESULT 998
ID ABL34228 standard; DNA; 8576 BP.
DE Human immune system associated gene SEQ ID NO: 2201.
PN WO200200928-A2.

PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 40; DB 6; Length 8576;
Best Local Similarity 49.1%; Pred. No. 7.6;
RESULT 999
ID ABL33418 standard; DNA; 10716 BP.
DE Human immune system associated gene SEQ ID NO: 1391.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 40; DB 6; Length 10716;
Best Local Similarity 49.1%; Pred. No. 8.8;
RESULT 1000
ID ABL33414 standard; DNA; 17389 BP.
DE Human immune system associated gene SEQ ID NO: 1387.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 40; DB 6; Length 17389;
Best Local Similarity 47.5%; Pred. No. 12;
RESULT 1001
ID ABL70604 standard; DNA; 34548 BP.
DE Chemically treated cell signalling DNA sequence complementary to#247.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 40; DB 6; Length 34548;
Best Local Similarity 49.1%; Pred. No. 19;
RESULT 1002
ID ABZ84585 standard; cDNA; 433 BP.
DE Toxicologically relevant human nucleotide sequence #1744.
PN WO2003016500-A2.
PD 27-FEB-2003.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 1.7%; Score 39.8; DB 10; Length 433;
Best Local Similarity 47.0%; Pred. No. 1.2;
RESULT 1003
ID ABZ13712 standard; DNA; 1371 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1517.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.7%; Score 39.8; DB 6; Length 1371;
Best Local Similarity 52.8%; Pred. No. 2.6;
RESULT 1004
ID ADG88170 standard; cDNA; 1371 BP.
DE A. thaliana RPP4-upregulated pathogen infection-related gene #612.
PN WO200222675-A2.
PD 21-MAR-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (UYN-) UNIV NORTH CAROLINA.
PA (GLAZ//) GLAZEBROOK J.
PA (WANG//) WANG X.
PA (DANG//) DANGL J L.
PA (EULG//) EULGEM T.
PA (ZHUT//) ZHU T.

Query Match 1.7%; Score 39.8; DB 6; Length 1371;
Best Local Similarity 52.8%; Pred. No. 2.6;
RESULT 1005
ID ACC49463 standard; cDNA; 1371 BP.
DE Arabidopsis glucosyltransferase 84B1 nucleic acid sequence.
PN WO2003023035-A2.
PD 20-MAR-2003.
PA (UYYO-) UNIV YORK.
Query Match 1.7%; Score 39.8; DB 8; Length 1371;
Best Local Similarity 53.5%; Pred. No. 2.6;
RESULT 1006
ID ADA69788 standard; DNA; 1407 BP.
DE Rice gene, SEQ ID 3111.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.7%; Score 39.8; DB 8; Length 1407;
Best Local Similarity 52.0%; Pred. No. 2.6;
RESULT 1007
ID ADJ40077 standard; cDNA; 1407 BP.
DE Plant cDNA #1077.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 1.7%; Score 39.8; DB 12; Length 1407;
Best Local Similarity 52.0%; Pred. No. 2.6;
RESULT 1008
ID AAD13660 standard; DNA; 1437 BP.
DE Arabidopsis thaliana glucosyltransferase (GTase) A911 gene.
PN WO200159140-A1.
PD 16-AUG-2001.
PA (UYYO-) UNIV YORK.
Query Match 1.7%; Score 39.8; DB 4; Length 1437;
Best Local Similarity 53.5%; Pred. No. 2.7;
RESULT 1009
ID AAD13680 standard; DNA; 1451 BP.
DE Arabidopsis thaliana glucosyltransferase (GTase) UGT76E1 DNA.
PN WO200159140-A1.
PD 16-AUG-2001.
PA (UYYO-) UNIV YORK.
Query Match 1.7%; Score 39.8; DB 4; Length 1451;
Best Local Similarity 52.8%; Pred. No. 2.7;
RESULT 1010
ID AAD13686 standard; DNA; 1494 BP.
DE Arabidopsis thaliana glucosyltransferase (GTase) UGT72B3 DNA.
PN WO200159140-A1.
PD 16-AUG-2001.

PA (UYYO-) UNIV YORK.
Query Match 1.7%; Score 39.8; DB 4; Length 1494;
Best Local Similarity 56.5%; Pred. No. 2.7;
RESULT 1011
ID AAC50671 standard; DNA; 1505 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 65708.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.7%; Score 39.8; DB 3; Length 1505;
Best Local Similarity 52.8%; Pred. No. 2.8;
RESULT 1012
ID ACC49460 standard; cDNA; 2559 BP.
DE Arabidopsis glucosyltransferase 74D1 nucleic acid sequence.
PN WO2003023035-A2.
PD 20-MAR-2003.
PA (UYYO-) UNIV YORK.
Query Match 1.7%; Score 39.8; DB 8; Length 2559;
Best Local Similarity 52.8%; Pred. No. 3.9;
RESULT 1013
ID AAA87491 standard; DNA; 273 BP.
DE Rat hepatocyte carcinogenesis biomarker nucleic acid SEQ ID NO:415.
PN WO200044902-A2.
PD 03-AUG-2000.
PA (SEAR) SEARLE & CO G D.
Query Match 1.7%; Score 39.6; DB 3; Length 273;
Best Local Similarity 48.8%; Pred. No. 1;
RESULT 1014
ID ADA69807 standard; DNA; 1419 BP.
DE Rice gene, SEQ ID 3130.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.7%; Score 39.6; DB 8; Length 1419;
Best Local Similarity 54.0%; Pred. No. 3;
RESULT 1015
ID AAD13681 standard; DNA; 1433 BP.
DE Arabidopsis thaliana glucosyltransferase (GTase) UGT76E11 DNA.
PN WO200159140-A1.
PD 16-AUG-2001.
PA (UYYO-) UNIV YORK.
Query Match 1.7%; Score 39.6; DB 4; Length 1433;
Best Local Similarity 54.9%; Pred. No. 3.1;
RESULT 1016
ID AAC51615 standard; DNA; 1594 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 69166.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.7%; Score 39.6; DB 3; Length 1594;
Best Local Similarity 54.9%; Pred. No. 3.3;
RESULT 1017
ID AAC39330 standard; DNA; 1596 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 24233.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.7%; Score 39.6; DB 3; Length 1596;
Best Local Similarity 54.9%; Pred. No. 3.3;
RESULT 1018

ID AAD55726 standard; DNA; 5858 BP.
DE *Nephila madagascariensis* major ampullate spidroin 2 (MaSp2)-like DNA.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Query Match 1.7%; Score 39.6; DB 8; Length 5858;
Best Local Similarity 46.9%; Pred. No. 7.8;
RESULT 1019

ID ABL33367 standard; DNA; 6104 BP.
DE Human immune system associated gene SEQ ID NO: 1340.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 39.6; DB 6; Length 6104;
Best Local Similarity 47.6%; Pred. No. 8;
RESULT 1020

ID ABL12934 standard; cDNA; 8004 BP.
DE *Drosophila melanogaster* expressed polynucleotide SEQ ID NO 33284.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.7%; Score 39.6; DB 4; Length 8004;
Best Local Similarity 45.5%; Pred. No. 9.6;
RESULT 1021

ID ABL12928 standard; cDNA; 8736 BP.
DE *Drosophila melanogaster* expressed polynucleotide SEQ ID NO 33266.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.7%; Score 39.6; DB 4; Length 8736;
Best Local Similarity 45.5%; Pred. No. 10;
RESULT 1022

ID AAS27804 standard; DNA; 31168 BP.
DE DNA encoding novel signal transduction pathway protein, Seq ID 1464.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.7%; Score 39.6; DB 4; Length 31168;
Best Local Similarity 56.0%; Pred. No. 24;
RESULT 1023

ID ABA07295 standard; DNA; 31168 BP.
DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 614.
PN WO200155206-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.7%; Score 39.6; DB 4; Length 31168;
Best Local Similarity 56.0%; Pred. No. 24;
RESULT 1024

ID AAS42115 standard; DNA; 31168 BP.
DE Genomic sequence #431 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.7%; Score 39.6; DB 4; Length 31168;
Best Local Similarity 56.0%; Pred. No. 24;
RESULT 1025

ID AAK89940 standard; DNA; 31168 BP.

DE Human digestive system antigen genomic sequence SEQ ID NO: 3516.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.7%; Score 39.6; DB 4; Length 31168;
Best Local Similarity 56.0%; Pred. No. 24;
RESULT 1026
ID AAK64760 standard; DNA; 31168 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19572.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.7%; Score 39.6; DB 4; Length 31168;
Best Local Similarity 56.0%; Pred. No. 24;
RESULT 1027
ID ADB94607 standard; DNA; 31168 BP.
DE Novel human protein DNA #216.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 1.7%; Score 39.6; DB 10; Length 31168;
Best Local Similarity 56.0%; Pred. No. 24;
RESULT 1028
ID AAA09469 standard; DNA; 50937 BP.
DE Streptococcus oleandomycin gene cluster.
PN WO200026349-A2.
PD 11-MAY-2000.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 1.7%; Score 39.6; DB 3; Length 50937;
Best Local Similarity 52.4%; Pred. No. 33;
RESULT 1029
Query Match 1.7%; Score 39.6; DB 8; Length 110000;
Best Local Similarity 61.8%; Pred. No. 55;
RESULT 1030
ID ADA68696 standard; DNA; 640 BP.
DE Rice gene, SEQ ID 2019.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.7%; Score 39.4; DB 8; Length 640;
Best Local Similarity 55.5%; Pred. No. 2.1;
RESULT 1031
ID AAD13666 standard; DNA; 1437 BP.
DE Arabidopsis thaliana glucosyltransferase (GTase) UGT71B5. DNA.
PN WO200159140-A1.
PD 16-AUG-2001.
PA (UYYO-) UNIV YORK.
Query Match 1.7%; Score 39.4; DB 4; Length 1437;
Best Local Similarity 52.8%; Pred. No. 3.5;
RESULT 1032
ID ADA68496 standard; DNA; 1437 BP.
DE Arabidopsis thaliana gene, SEQ ID 612.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.7%; Score 39.4; DB 8; Length 1437;
Best Local Similarity 52.8%; Pred. No. 3.5;
RESULT 1033
ID ABL05597 standard; cDNA; 1921 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 11273.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.7%; Score 39.4; DB 4; Length 1921;
Best Local Similarity 45.6%; Pred. No. 4.3;
RESULT 1034
ID ADL14347 standard; DNA; 1993 BP.
DE DNA encoding a carnation glycosyltransferase enzyme SeqID 16.
PN WO2004018682-A1.
PD 04-MAR-2004.
PA (SUNR) SUNTORY LTD.
PA (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.
Query Match 1.7%; Score 39.4; DB 12; Length 1993;
Best Local Similarity 52.8%; Pred. No. 4.4;
RESULT 1035
ID ABL05596 standard; cDNA; 4141 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 11270.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.7%; Score 39.4; DB 4; Length 4141;
Best Local Similarity 45.6%; Pred. No. 7.1;
RESULT 1036
ID ABN80023 standard; DNA; 6636 BP.
DE Human chemically modified disease associated gene SEQ ID NO 40.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 39.4; DB 6; Length 6636;
Best Local Similarity 46.8%; Pred. No. 9.7;
RESULT 1037
ID ABL32605 standard; DNA; 11155 BP.
DE Human immune system associated gene SEQ ID NO: 578.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 39.4; DB 6; Length 11155;
Best Local Similarity 51.5%; Pred. No. 14;
RESULT 1038
ID ABK31511 standard; DNA; 47108 BP.
DE Signal transduction associated gene modified complementary DNA #177.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 39.4; DB 6; Length 47108;
Best Local Similarity 48.4%; Pred. No. 36;
RESULT 1039
ID AAF65250 standard; cDNA; 378 BP.
DE Novel human polynucleotide, SEQ ID NO: 1006.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.

PA (HYSE-) HYSEQ INC.
Query Match 1.7%; Score 39.2; DB 5; Length 378;
Best Local Similarity 58.6%; Pred. No. 1.7;
RESULT 1040
ID ADM65498 standard; DNA; 482 BP.
DE NRY polymorphism detection primer #438.
PN US2003134285-A1.
PD 17-JUL-2003.
PA (OEFN/) OEFNER P J.
PA (UNDE/) UNDERHILL P A.
Query Match 1.7%; Score 39.2; DB 11; Length 482;
Best Local Similarity 55.0%; Pred. No. 2;
RESULT 1041
ID AAH53768 standard; DNA; 486 BP.
DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:2929.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 1.7%; Score 39.2; DB 4; Length 486;
Best Local Similarity 55.0%; Pred. No. 2;
RESULT 1042
ID ABN91345 standard; DNA; 492 BP.
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:808.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.7%; Score 39.2; DB 6; Length 492;
Best Local Similarity 55.0%; Pred. No. 2;
RESULT 1043
ID AAF08725 standard; cDNA; 578 BP.
DE Fusarium venenatum EST SEQ ID NO:1248.
PN WO200056762-A2.
PD 28-SEP-2000.
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO NORDISK AS.
Query Match 1.7%; Score 39.2; DB 3; Length 578;
Best Local Similarity 47.7%; Pred. No. 2.2;
RESULT 1044
ID ADJ12024 standard; DNA; 661 BP.
DE Wheat cDNA modulated by post-transcriptional gene silencing SeqID 660.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
Query Match 1.7%; Score 39.2; DB 11; Length 661;
Best Local Similarity 55.0%; Pred. No. 2.4;
RESULT 1045

ID AAC53614 standard; DNA; 1676 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 75115.
PN EP1033405-A2.
PD 06-SEP-2000.
 Query Match 1.7%; Score 39.2; DB 3; Length 1676;
 Best Local Similarity 51.7%; Pred. No. 4.5;
RESULT 1046
ID AAC54823 standard; DNA; 1676 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 79218.
PN EP1033405-A2.
PD 06-SEP-2000.
 Query Match 1.7%; Score 39.2; DB 3; Length 1676;
 Best Local Similarity 51.7%; Pred. No. 4.5;
RESULT 1047
ID AAH54132 standard; DNA; 3994 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3496.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
 Query Match 1.7%; Score 39.2; DB 4; Length 3994;
 Best Local Similarity 55.0%; Pred. No. 8;
RESULT 1048
ID ADJ43498 standard; cDNA; 503 BP.
DE Plant cDNA #4498.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
 Query Match 1.7%; Score 39; DB 12; Length 503;
 Best Local Similarity 55.6%; Pred. No. 2.3;
RESULT 1049
ID AAZ45117 standard; DNA; 759 BP.
DE UDP-glucuronosyltransferase 1 (UGT1) exon 1J nucleotide sequence.
PN WO9957322-A2.
PD 11-NOV-1999.
PA (AXYS-) AXYS PHARM INC.
 Query Match 1.7%; Score 39; DB 3; Length 759;
 Best Local Similarity 52.8%; Pred. No. 3;
RESULT 1050
ID AAZ45116 standard; DNA; 930 BP.
DE UDP-glucuronosyltransferase 1 (UGT1) exon 1H nucleotide sequence.
PN WO9957322-A2.
PD 11-NOV-1999.
PA (AXYS-) AXYS PHARM INC.
 Query Match 1.7%; Score 39; DB 3; Length 930;
 Best Local Similarity 52.8%; Pred. No. 3.5;
RESULT 1051
ID AAQ13726 standard; DNA; 1200 BP.

DE Zeaxanthin glycosylase - engineered.
PN WO9113078-A.
PD 05-SEP-1991.
PA (STAD) AMOCO CORP.
Query Match 1.7%; Score 39; DB 2; Length 1200;
Best Local Similarity 63.2%; Pred. No. 4.1;
RESULT 1052
ID AAD30176 standard; DNA; 1244 BP.
DE Human UDP-glucuronosyl transferase (UGT1A8) gene exon 1.
PN WO200206523-A2.
PD 24-JAN-2002.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 1.7%; Score 39; DB 6; Length 1244;
Best Local Similarity 52.8%; Pred. No. 4.2;
RESULT 1053
ID AAD30175 standard; DNA; 1452 BP.
DE Human UDP-glucuronosyl transferase (UGT1A10) gene exon 1.
PN WO200206523-A2.
PD 24-JAN-2002.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 1.7%; Score 39; DB 6; Length 1452;
Best Local Similarity 52.8%; Pred. No. 4.7;
RESULT 1054
ID ABL33154 standard; DNA; 5807 BP.
DE Human immune system associated gene SEQ ID NO: 1127.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 39; DB 6; Length 5807;
Best Local Similarity 48.8%; Pred. No. 12;
RESULT 1055
ID ABL33972 standard; DNA; 7771 BP.
DE Human immune system associated gene SEQ ID NO: 1945.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 39; DB 6; Length 7771;
Best Local Similarity 48.8%; Pred. No. 14;
RESULT 1056
ID ADM98599 standard; DNA; 12753 BP.
DE Geranylgeranyl pyrophosphate synthase DNA #19.
PN US2004072323-A1.
PD 15-APR-2004.
PA (MATS/) MATSUDA S P T.
PA (HART/) HART E A.
Query Match 1.7%; Score 39; DB 12; Length 12753;
Best Local Similarity 63.2%; Pred. No. 20;
RESULT 1057
ID ABA58871 standard; DNA; 478 BP.
DE Human foetal liver single exon nucleic acid probe #7176.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.7%; Score 38.8; DB 4; Length 478;
Best Local Similarity 47.2%; Pred. No. 2.6;
RESULT 1058
ID AAI38585 standard; DNA; 478 BP.

DE Probe #7271 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.7%; Score 38.8; DB 4; Length 478;
Best Local Similarity 47.2%; Pred. No. 2.6;
RESULT 1059
ID AAK32772 standard; DNA; 478 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 7329.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.7%; Score 38.8; DB 4; Length 478;
Best Local Similarity 47.2%; Pred. No. 2.6;
RESULT 1060
ID AAK07031 standard; DNA; 478 BP.
DE Human brain expressed single exon probe SEQ ID NO: 7022.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.7%; Score 38.8; DB 4; Length 478;
Best Local Similarity 47.2%; Pred. No. 2.6;
RESULT 1061
ID ABS32491 standard; DNA; 478 BP.
DE Human liver single exon probe, SEQ ID No 7481.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.7%; Score 38.8; DB 4; Length 478;
Best Local Similarity 47.2%; Pred. No. 2.6;
RESULT 1062
ID ABS07570 standard; DNA; 478 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 7561.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.7%; Score 38.8; DB 6; Length 478;
Best Local Similarity 47.2%; Pred. No. 2.6;
RESULT 1063
ID ADM65495 standard; DNA; 482 BP.
DE NRY polymorphism detection primer #436.
PN US2003134285-A1.
PD 17-JUL-2003.
PA (OEFN/) OEFNER P J.
PA (UNDE/) UNDERHILL P A.
Query Match 1.7%; Score 38.8; DB 11; Length 482;
Best Local Similarity 54.3%; Pred. No. 2.6;
RESULT 1064
ID ADJ12104 standard; DNA; 1134 BP.
DE Maize cDNA modulated by post-transcriptional gene silencing SeqID 740.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.

PA (GLAZ//) GLAZEBROOK J.
PA (GOFF//) GOFF S A.
PA (KATA//) KATAGIRI F.
PA (KREP//) KREPS J.
PA (MOUG//) MOUGHAMER T.
PA (PROV//) PROVART N.
PA (RICK//) RICKE D.
Query Match 1.7%; Score 38.8; DB 11; Length 1134;
Best Local Similarity 52.5%; Pred. No. 4.5;
RESULT 1065
ID ADJ44631 standard; cDNA; 1134 BP.
DE Plant cDNA #5631.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW//) BUDWORTH P.
PA (MOUG//) MOUGHAMER T.
PA (BRIG//) BRIGGS S P.
PA (COOP//) COOPER B.
PA (GLAZ//) GLAZEBROOK J.
PA (GOFF//) GOFF S A.
PA (KATA//) KATAGIRI F.
PA (KREP//) KREPS J.
PA (PROV//) PROVART N.
PA (RICK//) RICKE D.
PA (ZHUT//) ZHU T.
Query Match 1.7%; Score 38.8; DB 12; Length 1134;
Best Local Similarity 52.5%; Pred. No. 4.5;
RESULT 1066
ID ABL32539 standard; DNA; 5820 BP.
DE Human immune system associated gene SEQ ID NO: 512.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 38.8; DB 6; Length 5820;
Best Local Similarity 49.2%; Pred. No. 13;
RESULT 1067
ID ABL33758 standard; DNA; 7455 BP.
DE Human immune system associated gene SEQ ID NO: 1731.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 38.8; DB 6; Length 7455;
Best Local Similarity 46.9%; Pred. No. 16;
RESULT 1068
ID ABL32669 standard; DNA; 11049 BP.
DE Human immune system associated gene SEQ ID NO: 642.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 38.8; DB 6; Length 11049;
Best Local Similarity 54.1%; Pred. No. 21;
RESULT 1069
ID ABL92219 standard; DNA; 11049 BP.
DE Chemically treated DNA repair gene fragment complementary to#14.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.7%; Score 38.8; DB 6; Length 11049;
Best Local Similarity 54.1%; Pred. No. 21;
RESULT 1070
ID ABL49322 standard; DNA; 11049 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 22.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 38.8; DB 6; Length 11049;
Best Local Similarity 54.1%; Pred. No. 21;
RESULT 1071
ID ABL33900 standard; DNA; 11662 BP.
DE Human immune system associated gene SEQ ID NO: 1873.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 38.8; DB 6; Length 11662;
Best Local Similarity 48.2%; Pred. No. 21;
RESULT 1072
ID ADQ97617 standard; DNA; 57008 BP.
DE Human cancer associated sequence HD10-015, SEQ ID 594.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.7%; Score 38.8; DB 12; Length 57008;
Best Local Similarity 67.1%; Pred. No. 61;
RESULT 1073
ID ADK56217 standard; DNA; 640 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #3600.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 1.7%; Score 38.6; DB 10; Length 640;
Best Local Similarity 53.7%; Pred. No. 3.6;
RESULT 1074
ID ADC25996 standard; DNA; 1494 BP.
DE Oilseed rape UDP-glucosyltransferase DNA.
PN WO2003066836-A2.
PD 14-AUG-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.7%; Score 38.6; DB 10; Length 1494;
Best Local Similarity 53.7%; Pred. No. 6.3;
RESULT 1075
ID AAA70223 standard; DNA; 3549 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:356.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 1.7%; Score 38.6; DB 3; Length 3549;
Best Local Similarity 48.0%; Pred. No. 11;
RESULT 1076
ID ABN80086 standard; DNA; 7922 BP.
DE Human chemically modified disease associated gene SEQ ID NO 103.

PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 38.6; DB 6; Length 7922;
Best Local Similarity 50.3%; Pred. No. 19;
RESULT 1077
ID ADA47985 standard; DNA; 912 BP.
DE Rice gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.7%; Score 38.4; DB 9; Length 912;
Best Local Similarity 55.1%; Pred. No. 5.2;
RESULT 1078
ID AAQ33027 standard; DNA; 1667 BP.
DE Exon 5 from the UGT1 gene locus.
PN WO9212987-A1.
PD 06-AUG-1992.
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
Query Match 1.7%; Score 38.4; DB 2; Length 1667;
Best Local Similarity 48.2%; Pred. No. 7.7;
RESULT 1079
ID ABL02054 standard; cDNA; 4652 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 644.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.7%; Score 38.4; DB 4; Length 4652;
Best Local Similarity 52.5%; Pred. No. 15;
RESULT 1080
ID ABK28348 standard; DNA; 6076 BP.
DE DNA transcription associated complementary genomic DNA #111.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 38.4; DB 6; Length 6076;
Best Local Similarity 52.5%; Pred. No. 18;
RESULT 1081
ID AAA68075 standard; DNA; 330 BP.
DE Pinus radiata CGT nucleotide sequence SEQ ID NO:168.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 1.6%; Score 38.2; DB 3; Length 330;
Best Local Similarity 55.7%; Pred. No. 3;
RESULT 1082
ID ADD41825 standard; DNA; 330 BP.
DE Coniferol glucosyl transferase DNA #9.
PN US2003131373-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Query Match 1.6%; Score 38.2; DB 10; Length 330;
Best Local Similarity 55.7%; Pred. No. 3;
RESULT 1083
ID ADN74274 standard; cDNA; 1263 BP.

DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 2169.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 1.6%; Score 38.2; DB 12; Length 1263;
Best Local Similarity 50.3%; Pred. No. 7.4;
RESULT 1084
ID ADA69637 standard; DNA; 1460 BP.
DE Rice gene, SEQ ID 2960.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.6%; Score 38.2; DB 8; Length 1460;
Best Local Similarity 46.4%; Pred. No. 8.1;
RESULT 1085
ID ABL03434 standard; cDNA; 3633 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 4784.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.6%; Score 38.2; DB 4; Length 3633;
Best Local Similarity 50.8%; Pred. No. 15;
RESULT 1086
ID ABL03436 standard; cDNA; 3790 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 4790.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.6%; Score 38.2; DB 4; Length 3790;
Best Local Similarity 50.8%; Pred. No. 15;
RESULT 1087
ID ADK56219 standard; DNA; 651 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #3602.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 1.6%; Score 38; DB 10; Length 651;
Best Local Similarity 53.3%; Pred. No. 5.5;
RESULT 1088
ID ADA68497 standard; DNA; 1359 BP.
DE Arabidopsis thaliana gene, SEQ ID 613.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.6%; Score 37.8; DB 8; Length 1359;
Best Local Similarity 52.2%; Pred. No. 10;
RESULT 1089
ID ABK33919 standard; DNA; 7001 BP.
DE Human DNA for staging of Astrocytomas #1.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37.8; DB 6; Length 7001;
Best Local Similarity 48.4%; Pred. No. 30;
RESULT 1090
ID ADA20394 standard; DNA; 7001 BP.

DE Prostate tumour related genomic DNA sample #30.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37.8; DB 8; Length 7001;
Best Local Similarity 48.4%; Pred. No. 30;
RESULT 1091
ID ADA84201 standard; DNA; 7001 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:59.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37.8; DB 8; Length 7001;
Best Local Similarity 48.4%; Pred. No. 30;
RESULT 1092
ID ABA81167 standard; DNA; 121 BP.
DE UGT1 mutation correcting oligonucleotide SEQ ID NO: 4013.
PN WO200173002-A2.
PD 04-OCT-2001.
PA (UYDE) UNIV DELAWARE.
Query Match 1.6%; Score 37.6; DB 4; Length 121;
Best Local Similarity 59.3%; Pred. No. 2.3;
RESULT 1093
ID ABA81166 standard; DNA; 121 BP.
DE UGT1 mutation correcting oligonucleotide SEQ ID NO: 4012.
PN WO200173002-A2.
PD 04-OCT-2001.
PA (UYDE) UNIV DELAWARE.
Query Match 1.6%; Score 37.6; DB 4; Length 121;
Best Local Similarity 59.3%; Pred. No. 2.3;
RESULT 1094
ID ADM65492 standard; DNA; 482 BP.
DE NRY polymorphism detection primer #434.
PN US2003134285-A1.
PD 17-JUL-2003.
PA (OEFN/) OEFNER P J.
PA (UNDE/) UNDERHILL P A.
Query Match 1.6%; Score 37.6; DB 11; Length 482;
Best Local Similarity 54.3%; Pred. No. 5.9;
RESULT 1095
ID ADI81801 standard; cDNA; 492 BP.
DE A. thaliana array-associated cDNA SEQ ID 3.
PN DE10204843-A1.
PD 14-AUG-2003.
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
Query Match 1.6%; Score 37.6; DB 10; Length 492;
Best Local Similarity 55.3%; Pred. No. 6;
RESULT 1096
ID AAC67675 standard; cDNA; 1092 BP.
DE Human secreted protein cDNA sequence #45.
PN WO200058355-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 37.6; DB 3; Length 1092;
Best Local Similarity 50.6%; Pred. No. 10;
RESULT 1097
ID ACA31552 standard; DNA; 1575 BP.

DE Prokaryotic essential gene #13209.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.6%; Score 37.6; DB 8; Length 1575;
Best Local Similarity 50.6%; Pred. No. 13;
RESULT 1098
ID ABL33217 standard; DNA; 6191 BP.
DE Human immune system associated gene SEQ ID NO: 1190.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37.6; DB 6; Length 6191;
Best Local Similarity 49.0%; Pred. No. 32;
RESULT 1099
ID ABK31307 standard; DNA; 6191 BP.
DE Signal transduction associated gene modified complementary DNA #75.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37.6; DB 6; Length 6191;
Best Local Similarity 49.0%; Pred. No. 32;
RESULT 1100
ID ABL70282 standard; DNA; 6191 BP.
DE Chemically treated cell signalling DNA sequence complementary to#86.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37.6; DB 6; Length 6191;
Best Local Similarity 49.0%; Pred. No. 32;
RESULT 1101
ID ABN80161 standard; DNA; 6191 BP.
DE Human chemically modified disease associated gene SEQ ID NO 178.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37.6; DB 6; Length 6191;
Best Local Similarity 49.0%; Pred. No. 32;
RESULT 1102
ID ABL33825 standard; DNA; 8771 BP.
DE Human immune system associated gene SEQ ID NO: 1798.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37.6; DB 6; Length 8771;
Best Local Similarity 46.0%; Pred. No. 40;
RESULT 1103
ID ACN44838 standard; DNA; 54169 BP.
DE Human genomic sequence hCG1766501.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.6%; Score 37.6; DB 11; Length 54169;
Best Local Similarity 45.3%; Pred. No. 1.4e+02;
RESULT 1104
Query Match 1.6%; Score 37.6; DB 2; Length 110000;
Best Local Similarity 47.1%; Pred. No. 2.2e+02;

RESULT 1105
ID ADH58564 standard; DNA; 139573 BP.
DE Human Na⁺-independent transporter-related transporter protein gene.
Query Match 1.6%; Score 37.6; DB 10; Length 139573;
Best Local Similarity 48.6%; Pred. No. 2.5e+02;
RESULT 1106
ID ABD32817 standard; DNA; 156416 BP.
DE Human cancer-associated genomic DNA HD17-001.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.6%; Score 37.6; DB 13; Length 156416;
Best Local Similarity 48.6%; Pred. No. 2.7e+02;
RESULT 1107
ID ACH76814 standard; DNA; 526 BP.
DE Human genome derived single exon probe #10009.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 1.6%; Score 37.4; DB 12; Length 526;
Best Local Similarity 52.2%; Pred. No. 7.1;
RESULT 1108
ID ACA22952 standard; DNA; 882 BP.
DE Prokaryotic essential gene #4609.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.6%; Score 37.4; DB 8; Length 882;
Best Local Similarity 60.2%; Pred. No. 10;
RESULT 1109
ID AAD55027 standard; DNA; 1365 BP.
DE Tulip pistil UDP-glucosyltransferase homologue gene, 114.
PN WO2002101013-A2.
PD 19-DEC-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PRAB/) PRABHU V.
Query Match 1.6%; Score 37.4; DB 10; Length 1365;
Best Local Similarity 53.8%; Pred. No. 13;
RESULT 1110
ID ABZ13579 standard; DNA; 1368 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1384.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.6%; Score 37.4; DB 6; Length 1368;
Best Local Similarity 53.0%; Pred. No. 13;
RESULT 1111
ID ADG87648 standard; cDNA; 1368 BP.
DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #90.
PN WO200222675-A2.
PD 21-MAR-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (UYNM-) UNIV NORTH CAROLINA.
PA (GLAZ/) GLAZEBROOK J.

PA (WANG/) WANG X.
PA (DANG/) DANGL J L.
PA (EULG/) EULGEM T.
PA (ZHUT/) ZHU T.
Query Match 1.6%; Score 37.4; DB 6; Length 1368;
Best Local Similarity 53.0%; Pred. No. 13;
RESULT 1112
ID ADG88159 standard; cDNA; 1368 BP.
DE A. thaliana RPP4-upregulated pathogen infection-related gene #601.
PN WO200222675-A2.
PD 21-MAR-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (UYNC-) UNIV NORTH CAROLINA.
PA (GLAZ/) GLAZEBROOK J.
PA (WANG/) WANG X.
PA (DANG/) DANGL J L.
PA (EULG/) EULGEM T.
PA (ZHUT/) ZHU T.
Query Match 1.6%; Score 37.4; DB 6; Length 1368;
Best Local Similarity 53.0%; Pred. No. 13;
RESULT 1113
ID ADG87823 standard; cDNA; 1368 BP.
DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #265.
PN WO200222675-A2.
PD 21-MAR-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (UYNC-) UNIV NORTH CAROLINA.
PA (GLAZ/) GLAZEBROOK J.
PA (WANG/) WANG X.
PA (DANG/) DANGL J L.
PA (EULG/) EULGEM T.
PA (ZHUT/) ZHU T.
Query Match 1.6%; Score 37.4; DB 6; Length 1368;
Best Local Similarity 53.0%; Pred. No. 13;
RESULT 1114
ID ADA68049 standard; DNA; 1368 BP.
DE Arabidopsis thaliana gene, SEQ ID 304.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.6%; Score 37.4; DB 8; Length 1368;
Best Local Similarity 53.0%; Pred. No. 13;
RESULT 1115
ID AAD13669 standard; DNA; 1404 BP.
DE Arabidopsis thaliana glucosyltransferase (GTase) UGT71D1 DNA.
PN WO200159140-A1.
PD 16-AUG-2001.
PA (UYYO-) UNIV YORK.
Query Match 1.6%; Score 37.4; DB 4; Length 1404;
Best Local Similarity 51.5%; Pred. No. 14;
RESULT 1116
ID ABZ14405 standard; DNA; 1404 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2210.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.6%; Score 37.4; DB 6; Length 1404;
Best Local Similarity 51.5%; Pred. No. 14;
RESULT 1117

ID AAC42644 standard; DNA; 1556 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36326.
PN EP1033405-A2.
PD 06-SEP-2000.

Query Match 1.6%; Score 37.4; DB 3; Length 1556;
Best Local Similarity 51.5%; Pred. No. 15;
RESULT 1118

ID ACA48184 standard; DNA; 2127 BP.
DE Prokaryotic essential gene #29841.
PN WO200277183-A2.
PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.
Query Match 1.6%; Score 37.4; DB 8; Length 2127;
Best Local Similarity 50.9%; Pred. No. 18;
RESULT 1119

ID AAX84332 standard; DNA; 5059 BP.
DE Stealth virus nucleic acid clone, SEQ ID NO: 24.
Query Match 1.6%; Score 37.4; DB 2; Length 5059;
Best Local Similarity 12.9%; Pred. No. 32;
RESULT 1120

ID AAC76580 standard; cDNA; 5748 BP.
DE Human ORFX ORF2135 polynucleotide sequence SEQ ID NO: 4269.
PN WO200058473-A2.
PD 05-OCT-2000.

PA (CURA-) CURAGEN CORP.
Query Match 1.6%; Score 37.4; DB 3; Length 5748;
Best Local Similarity 49.2%; Pred. No. 35;
RESULT 1121

ID AAH98460 standard; cDNA; 6248 BP.
DE Murine EST-derived coding sequence SEQ ID NO: 317.
PN WO200154477-A2.
PD 02-AUG-2001.

PA (HYSE-) HYSEQ INC.
Query Match 1.6%; Score 37.4; DB 4; Length 6248;
Best Local Similarity 49.2%; Pred. No. 37;
RESULT 1122

ID AAS20800 standard; DNA; 48551 BP.
DE Clostridium difficile DNA sequence upstream of ORF1.
PN WO200194599-A1.
PD 13-DEC-2001.

PA (SMIT-) SMITTSKYDDSINSTITUTET.
Query Match 1.6%; Score 37.4; DB 6; Length 48551;
Best Local Similarity 53.0%; Pred. No. 1.4e+02;
RESULT 1123

Query Match 1.6%; Score 37.4; DB 2; Length 110000;
Best Local Similarity 60.2%; Pred. No. 2.5e+02;
RESULT 1124

ID AAH71505 standard; cDNA; 310 BP.
DE Human cervical cancer marker nucleic acid 2779.
PN WO200142467-A2.
PD 14-JUN-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.6%; Score 37.2; DB 4; Length 310;
Best Local Similarity 53.4%; Pred. No. 5.8;

RESULT 1125

ID ADA68697 standard; DNA; 843 BP.

DE Rice gene, SEQ ID 2020.

PN WO2003000898-A1.

PD 03-JAN-2003.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.6%; Score 37.2; DB 8; Length 843;

Best Local Similarity 59.4%; Pred. No. 11;

RESULT 1126

ID ADJ11669 standard; DNA; 1110 BP.

DE Rice DNA modulated by post-transcriptional gene silencing SeqID 305.

PN US2003135888-A1.

PD 17-JUL-2003.

PA (ZHUT/) ZHU T.

PA (WANG/) WANG X.

PA (CHAN/) CHANG H.

PA (BRIG/) BRIGGS S P.

PA (COOP/) COOPER B.

PA (GLAZ/) GLAZEBROOK J.

PA (GOFF/) GOFF S A.

PA (KATA/) KATAGIRI F.

PA (KREP/) KREPS J.

PA (MOUG/) MOUGHAMER T.

PA (PROV/) PROVART N.

PA (RICK/) RICKE D.

Query Match 1.6%; Score 37.2; DB 11; Length 1110;

Best Local Similarity 55.4%; Pred. No. 13;

RESULT 1127

ID AAV23108 standard; cDNA to mRNA; 1597 BP.

DE UDP-glucose:flavonoid 3,5-O-glucosyl transferase gene.

PN JP10113184-A.

PD 06-MAY-1998.

PA (TOLG) TOKYO GAS CO LTD.

Query Match 1.6%; Score 37.2; DB 2; Length 1597;

Best Local Similarity 54.3%; Pred. No. 17;

RESULT 1128

ID ADJ75971 standard; DNA; 2779 BP.

DE Marker gene SEQ ID NO:1223.

PN EP1394274-A2.

PD 03-MAR-2004.

PA (GENO-) GENOX RES INC.

Query Match 1.6%; Score 37.2; DB 12; Length 2779;

Best Local Similarity 47.8%; Pred. No. 25;

RESULT 1129

ID ACA47967 standard; DNA; 3502 BP.

DE Prokaryotic essential gene #29624.

PN WO200277183-A2.

PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.

Query Match 1.6%; Score 37.2; DB 8; Length 3502;

Best Local Similarity 61.2%; Pred. No. 29;

RESULT 1130

ID ADM01769 standard; cDNA; 3524 BP.

DE Human cDNA of the invention SEQ ID NO:454.

PN EP1347046-A1.

PD 24-SEP-2003.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Query Match 1.6%; Score 37.2; DB 11; Length 3524;
Best Local Similarity 56.6%; Pred. No. 29;
RESULT 1131
ID ABL05102 standard; cDNA; 3992 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 9788.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.6%; Score 37.2; DB 4; Length 3992;
Best Local Similarity 61.2%; Pred. No. 31;
RESULT 1132
ID ACN44838 standard; DNA; 54169 BP.
DE Human genomic sequence hCG1766501.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.6%; Score 37.2; DB 11; Length 54169;
Best Local Similarity 51.2%; Pred. No. 1.8e+02;
RESULT 1133
ID ADD67054 standard; cDNA; 161280 BP.
DE Human lung tumour-specific related cDNA, SEQ ID No 746.
PN WO200292001-A2.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 37.2; DB 10; Length 161280;
Best Local Similarity 51.9%; Pred. No. 3.7e+02;
RESULT 1134
ID ADE88308 standard; cDNA; 161280 BP.
DE Human lung tumour antigen cDNA #640.
PN US2003118599-A1.
PD 26-JUN-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 37.2; DB 10; Length 161280;
Best Local Similarity 51.9%; Pred. No. 3.7e+02;
RESULT 1135
ID AAC74529 standard; cDNA; 510 BP.
DE Human ORFX ORF84 polynucleotide sequence SEQ ID NO:167.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 1.6%; Score 37; DB 3; Length 510;
Best Local Similarity 53.9%; Pred. No. 9.2;
RESULT 1136
ID ABX57387 standard; DNA; 537 BP.
DE Arabidopsis thaliana polynucleotide #739.
PN US2002040489-A1.
PD 04-APR-2002.
PA (GORL/) GORLACH J.
PA (ANYY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.

PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.

Query Match 1.6%; Score 37; DB 10; Length 537;
Best Local Similarity 54.9%; Pred. No. 9.5;

RESULT 1137

ID ADK52732 standard; DNA; 753 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #115.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.

Query Match 1.6%; Score 37; DB 10; Length 753;
Best Local Similarity 54.9%; Pred. No. 12;

RESULT 1138

ID AAD55026 standard; DNA; 1365 BP.
DE Tulip pistil UDP-glucosyltransferase homologue gene, n21.
PN WO2002101013-A2.
PD 19-DEC-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PRAB/) PRABHU V.

Query Match 1.6%; Score 37; DB 10; Length 1365;
Best Local Similarity 53.9%; Pred. No. 18;

RESULT 1139

ID ABZ14007 standard; DNA; 1446 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1812.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.6%; Score 37; DB 6; Length 1446;
Best Local Similarity 54.9%; Pred. No. 18;

RESULT 1140

ID AAV49609 standard; cDNA; 1607 BP.
DE Potato solanidine UDP-glucose glucosyltransferase cDNA.
PN WO9834471-A1.
PD 13-AUG-1998.
PA (USDA) US SEC OF AGRIC.

Query Match 1.6%; Score 37; DB 2; Length 1607;
Best Local Similarity 48.0%; Pred. No. 20;

RESULT 1141

ID ADL14386 standard; DNA; 1670 BP.
DE DNA encoding a carnation glycosyltransferase enzyme SeqID 55.
PN WO2004018682-A1.
PD 04-MAR-2004.
PA (SUNR) SUNTORY LTD.
PA (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.

Query Match 1.6%; Score 37; DB 12; Length 1670;
Best Local Similarity 53.0%; Pred. No. 20;

RESULT 1142

ID AAS15727 standard; cDNA; 2145 BP.

DE DNA encoding sulfate anion transporter family related protein, NOV7.
PN WO200170978-A2.
PD 27-SEP-2001.
PA (CURA-) CURAGEN CORP.
Query Match 1.6%; Score 37; DB 4; Length 2145;
Best Local Similarity 53.9%; Pred. No. 24;
RESULT 1143
ID ADJ87760 standard; DNA; 2145 BP.
DE G-coupled protein receptor-related protein coding sequence #53.
PN WO2002102321-A2.
PD 27-DEC-2002.
PA (CURA-) CURAGEN CORP.
Query Match 1.6%; Score 37; DB 10; Length 2145;
Best Local Similarity 53.9%; Pred. No. 24;
RESULT 1144
ID ADO55995 standard; cDNA; 2145 BP.
DE DNA encoding human NOV7.
PN US2004058862-A1.
PD 25-MAR-2004.
PA (MAJU/) MAJUMDER K.
Query Match 1.6%; Score 37; DB 12; Length 2145;
Best Local Similarity 53.9%; Pred. No. 24;
RESULT 1145
ID AAD33658 standard; cDNA; 2600 BP.
DE Human TRICH-13 cDNA.
PN WO200212340-A2.
PD 14-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.6%; Score 37; DB 6; Length 2600;
Best Local Similarity 53.9%; Pred. No. 27;
RESULT 1146
ID AAL44757 standard; cDNA; 3435 BP.
DE Human transporter protein cDNA.
PN WO200188136-A2.
PD 22-NOV-2001.
PA (APPL-) APPLERA CORP.
Query Match 1.6%; Score 37; DB 6; Length 3435;
Best Local Similarity 53.9%; Pred. No. 33;
RESULT 1147
ID ABL33772 standard; DNA; 5666 BP.
DE Human immune system associated gene SEQ ID NO: 1745.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37; DB 6; Length 5666;
Best Local Similarity 53.9%; Pred. No. 46;
RESULT 1148
ID ABL33386 standard; DNA; 8064 BP.
DE Human immune system associated gene SEQ ID NO: 1359.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37; DB 6; Length 8064;
Best Local Similarity 53.0%; Pred. No. 58;
RESULT 1149
ID AAL44758 standard; DNA; 8868 BP.
DE Human transporter protein gene.

PN WO200188136-A2.
PD 22-NOV-2001.
PA (APPL-) APPLERA CORP.
 Query Match 1.6%; Score 37; DB 6; Length 8868;
 Best Local Similarity 53.9%; Pred. No. 61;
RESULT 1150
ID AAK71442 standard; DNA; 23934 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26254.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.6%; Score 37; DB 4; Length 23934;
 Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1151
ID AAL36171 standard; DNA; 23934 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2536.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.6%; Score 37; DB 4; Length 23934;
 Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1152
ID AAL36179 standard; DNA; 23934 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2544.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.6%; Score 37; DB 4; Length 23934;
 Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1153
ID AAL04522 standard; DNA; 23934 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7210.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.6%; Score 37; DB 4; Length 23934;
 Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1154
ID AAS28343 standard; DNA; 23934 BP.
DE Genomic sequence #183 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.6%; Score 37; DB 4; Length 23934;
 Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1155
ID ABL97446 standard; DNA; 23934 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2098.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.6%; Score 37; DB 4; Length 23934;
 Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1156
ID ABA19145 standard; DNA; 23934 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11476.
PN WO200159063-A2.

PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 37; DB 5; Length 23934;
Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1157
ID ABX59167 standard; cDNA; 23934 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1511.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 1.6%; Score 37; DB 8; Length 23934;
Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1158
ID ABX59159 standard; cDNA; 23934 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1503.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 1.6%; Score 37; DB 8; Length 23934;
Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1159
ID ADG41539 standard; DNA; 23934 BP.
DE Human respiratory system associated genomic DNA seq id 777.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 37; DB 10; Length 23934;
Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1160
ID ADI97313 standard; DNA; 23934 BP.
DE Human respiratory system associated polypeptide-related DNA SeqID777.
PN US2003077704-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 37; DB 11; Length 23934;
Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1161
ID ADJ29917 standard; DNA; 23934 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2544.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 37; DB 12; Length 23934;
Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1162
ID ADJ29909 standard; DNA; 23934 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2536.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 37; DB 12; Length 23934;
Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1163

Query Match 1.6%; Score 37; DB 13; Length 110000;
Best Local Similarity 49.7%; Pred. No. 3.3e+02;
RESULT 1164
ID ADB50767 standard; DNA; 512 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:1309.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 1.6%; Score 36.8; DB 10; Length 512;
Best Local Similarity 50.6%; Pred. No. 11;
RESULT 1165
ID ABV57126 standard; cDNA; 550 BP.
DE Human prostate expression marker cDNA 57117.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.6%; Score 36.8; DB 5; Length 550;
Best Local Similarity 51.9%; Pred. No. 11;
RESULT 1166
ID AAT87010 standard; DNA; 618 BP.
DE Nitrile hydratase alpha 29 kDa subunit encoding DNA.
PN EP790310-A2.
PD 20-AUG-1997.
PA (MITK) MITSUI TOATSU CHEM INC.
Query Match 1.6%; Score 36.8; DB 2; Length 618;
Best Local Similarity 51.2%; Pred. No. 12;
RESULT 1167
ID ADP82951 standard; DNA; 618 BP.
DE Nitrile hydratase alpha subunit coding sequence, SEQ ID 3.
PN WO2004056990-A1.
PD 08-JUL-2004.
PA (MITA) MITSUI CHEM INC.
Query Match 1.6%; Score 36.8; DB 12; Length 618;
Best Local Similarity 51.2%; Pred. No. 12;
RESULT 1168
ID ADP83048 standard; DNA; 618 BP.
DE Nitrile hydratase alpha subunit coding sequence, SEQ ID 100.
PN WO2004056990-A1.
PD 08-JUL-2004.
PA (MITA) MITSUI CHEM INC.
Query Match 1.6%; Score 36.8; DB 12; Length 618;
Best Local Similarity 51.2%; Pred. No. 12;
RESULT 1169
ID AAZ95194 standard; DNA; 746 BP.
DE Human UGT2B4 exon 2 nucleotide sequence.
PN WO200006776-A1.
PD 10-FEB-2000.
PA (AXYS-) AXYS PHARM INC.
Query Match 1.6%; Score 36.8; DB 3; Length 746;
Best Local Similarity 54.4%; Pred. No. 14;
RESULT 1170
ID AAD49417 standard; DNA; 936 BP.
DE Human serine/threonine protein kinase-like protein (STPKP) DNA #2.
PN WO200283882-A2.
PD 24-OCT-2002.
PA (FARB) BAYER AG.
Query Match 1.6%; Score 36.8; DB 8; Length 936;

Best Local Similarity 56.7%; Pred. No. 16;
RESULT 1171
ID AAH51490 standard; DNA; 1001 BP.
DE Human UGT2B4 related DNA containing a biallelic polymorphism SEQ ID 381.
PN WO200058508-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 1.6%; Score 36.8; DB 3; Length 1001;
Best Local Similarity 54.4%; Pred. No. 17;
RESULT 1172
ID AAH51491 standard; DNA; 1001 BP.
DE Human UGT2B4 related DNA containing a biallelic polymorphism SEQ ID 382.
PN WO200058508-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 1.6%; Score 36.8; DB 3; Length 1001;
Best Local Similarity 54.4%; Pred. No. 17;
RESULT 1173
ID AAD49416 standard; DNA; 1272 BP.
DE Human serine/threonine protein kinase-like protein (STPKP) DNA #1.
PN WO200283882-A2.
PD 24-OCT-2002.
PA (FARB) BAYER AG.
Query Match 1.6%; Score 36.8; DB 8; Length 1272;
Best Local Similarity 56.7%; Pred. No. 19;
RESULT 1174
ID AAS06744 standard; cDNA; 1275 BP.
DE Polynucleotide sequence encoding human protein kinase #44.
PN WO200138503-A2.
PD 31-MAY-2001.
PA (SUGE-) SUGEN INC.
Query Match 1.6%; Score 36.8; DB 4; Length 1275;
Best Local Similarity 56.7%; Pred. No. 19;
RESULT 1175
ID AAD49419 standard; DNA; 1275 BP.
DE Human serine/threonine protein kinase-like protein (STPKP) DNA #4.
PN WO200283882-A2.
PD 24-OCT-2002.
PA (FARB) BAYER AG.
Query Match 1.6%; Score 36.8; DB 8; Length 1275;
Best Local Similarity 56.7%; Pred. No. 19;
RESULT 1176
ID ABD33093 standard; cDNA; 1282 BP.
DE Human cancer-associated (CA) cDNA HR07-006.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.6%; Score 36.8; DB 13; Length 1282;
Best Local Similarity 56.7%; Pred. No. 20;
RESULT 1177
ID AAH68614 standard; cDNA; 1441 BP.
DE Human protein HP10580 coding sequence.
PN WO200142302-A1.
PD 14-JUN-2001.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 1.6%; Score 36.8; DB 5; Length 1441;
Best Local Similarity 44.9%; Pred. No. 21;

RESULT 1178

ID ABK86975 standard; cDNA; 1473 BP.
DE Novel human protein (NHP) coding DNA.
PN WO200246428-A2.
PD 13-JUN-2002.
PA (LEXI-) LEXICON GENETICS INC.

Query Match 1.6%; Score 36.8; DB 6; Length 1473;
Best Local Similarity 56.7%; Pred. No. 21;

RESULT 1179

ID ACA37821 standard; DNA; 1650 BP.
DE Prokaryotic essential gene #19478.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

Query Match 1.6%; Score 36.8; DB 8; Length 1650;
Best Local Similarity 58.0%; Pred. No. 23;

RESULT 1180

ID ADQ85655 standard; cDNA; 1656 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2469.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.

Query Match 1.6%; Score 36.8; DB 12; Length 1656;
Best Local Similarity 44.9%; Pred. No. 23;

RESULT 1181

ID ADQ84269 standard; cDNA; 1656 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1083.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.

Query Match 1.6%; Score 36.8; DB 12; Length 1656;
Best Local Similarity 44.9%; Pred. No. 23;

RESULT 1182

ID ADQ86749 standard; cDNA; 1656 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3624.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.

Query Match 1.6%; Score 36.8; DB 13; Length 1656;
Best Local Similarity 44.9%; Pred. No. 23;

RESULT 1183

ID ACN40421 standard; cDNA; 1656 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326536, SEQ ID NO:5190.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.

Query Match 1.6%; Score 36.8; DB 13; Length 1656;
Best Local Similarity 44.9%; Pred. No. 23;

RESULT 1184

ID AAZ09324 standard; DNA; 1762 BP.
DE P. thermophila nitrilase DNA.

PN EP943686-A2.
PD 22-SEP-1999.
PA (MITA) MITSUI CHEM INC.
Query Match 1.6%; Score 36.8; DB 2; Length 1762;
Best Local Similarity 51.2%; Pred. No. 24;
RESULT 1185
ID AAH64962 standard; cDNA; 1829 BP.
DE Human secreted protein cDNA, SEQ ID NO: 238.
PN WO200142451-A2.
PD 14-JUN-2001.
PA (GEST) GENSET.
Query Match 1.6%; Score 36.8; DB 5; Length 1829;
Best Local Similarity 44.9%; Pred. No. 25;
RESULT 1186
ID ACC00697 standard; cDNA; 1874 BP.
DE Triticum aestivum oil trait related cDNA sequence SEQ ID NO:143.
PN WO2003002751-A2.
PD 09-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 1.6%; Score 36.8; DB 8; Length 1874;
Best Local Similarity 51.9%; Pred. No. 25;
RESULT 1187
ID ADC23622 standard; cDNA; 1874 BP.
DE cDNA encodes protein used to alter plant oil phenotype (SeqID 127).
PN WO2003001902-A2.
PD 09-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 1.6%; Score 36.8; DB 10; Length 1874;
Best Local Similarity 51.9%; Pred. No. 25;
RESULT 1188
ID ABX34648 standard; cDNA; 1960 BP.
DE Human mddt cDNA SEQ ID 209.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.6%; Score 36.8; DB 8; Length 1960;
Best Local Similarity 44.9%; Pred. No. 26;
RESULT 1189
ID AAD34298 standard; cDNA; 2060 BP.
DE Human PKIN-1 cDNA.
PN WO200218557-A2.
PD 07-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.6%; Score 36.8; DB 6; Length 2060;....
Best Local Similarity 56.7%; Pred. No. 27;
RESULT 1190
ID ACA37512 standard; DNA; 2196 BP.
DE Prokaryotic essential gene #19169.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.6%; Score 36.8; DB 8; Length 2196;
Best Local Similarity 48.1%; Pred. No. 28;
RESULT 1191
ID AAS17862 standard; cDNA; 2598 BP.

DE Human protein kinase N cDNA.
PN WO200188148-A2.
PD 22-NOV-2001.
PA (APPL-) APPLERA CORP.
Query Match 1.6%; Score 36.8; DB 6; Length 2598;
Best Local Similarity 56.7%; Pred. No. 31;
RESULT 1192
ID ABK10101 standard; cDNA; 2893 BP.
DE Human cDNA encoding protein kinase 32374.
PN WO200210401-A2.
PD 07-FEB-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.6%; Score 36.8; DB 6; Length 2893;
Best Local Similarity 56.7%; Pred. No. 33;
RESULT 1193
ID AAD49420 standard; DNA; 3124 BP.
DE Human serine/threonine protein kinase-like protein (STPKP) DNA #5.
PN WO200283882-A2.
PD 24-OCT-2002.
PA (FARB) BAYER AG.
Query Match 1.6%; Score 36.8; DB 8; Length 3124;
Best Local Similarity 56.7%; Pred. No. 35;
RESULT 1194
ID ADS89626 standard; DNA; 3862 BP.
DE Oligonucleotide of the invention SEQ ID NO:642.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.8; DB 13; Length 3862;
Best Local Similarity 49.5%; Pred. No. 41;
RESULT 1195
ID AAS63343 standard; DNA; 5464 BP.
DE Chemically pretreated metabolism associated gene #38.
PN WO200176451-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.8; DB 6; Length 5464;
Best Local Similarity 55.5%; Pred. No. 51;
RESULT 1196
ID AAA70152 standard; DNA; 6033 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:285.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 1.6%; Score 36.8; DB 3; Length 6033;
Best Local Similarity 53.5%; Pred. No. 55;
RESULT 1197
ID ABL32369 standard; DNA; 9997 BP.
DE Human immune system associated gene SEQ ID NO: 342.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.8; DB 6; Length 9997;
Best Local Similarity 46.8%; Pred. No. 76;

RESULT 1198
ID ABL34485 standard; DNA; 9997 BP.
DE Human metastasis associated gene SEQ ID NO: 38.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.8; DB 6; Length 9997;
Best Local Similarity 46.8%; Pred. No. 76;
RESULT 1199
ID ADS99746 standard; DNA; 9997 BP.
DE Complement of bisulphite treated metastasis-associated human gene #19.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 1.6%; Score 36.8; DB 7; Length 9997;
Best Local Similarity 46.8%; Pred. No. 76;
RESULT 1200
ID ABL33075 standard; DNA; 10254 BP.
DE Human immune system associated gene SEQ ID NO: 1048.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.8; DB 6; Length 10254;
Best Local Similarity 47.4%; Pred. No. 78;
RESULT 1201
ID ABL33262 standard; DNA; 12393 BP.
DE Human immune system associated gene SEQ ID NO: 1235.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.8; DB 6; Length 12393;
Best Local Similarity 50.0%; Pred. No. 88;
RESULT 1202
ID AAS45349 standard; DNA; 17421 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #27.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.8; DB 4; Length 17421;
Best Local Similarity 51.2%; Pred. No. 1.1e+02;
RESULT 1203
ID ABK28182 standard; DNA; 17421 BP.
DE DNA transcription associated complementary genomic DNA #28.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.8; DB 6; Length 17421;
Best Local Similarity 51.2%; Pred. No. 1.1e+02;
RESULT 1204
ID ABQ67059 standard; DNA; 34688 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 89.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.8; DB 6; Length 34688;

Best Local Similarity 50.6%; Pred. No. 1.7e+02;
RESULT 1205
ID ABL34125 standard; DNA; 73334 BP.
DE Human immune system associated gene SEQ ID NO: 2098.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.8; DB 6; Length 73334;
Best Local Similarity 48.2%; Pred. No. 2.9e+02;
RESULT 1206
ID ABL92319 standard; DNA; 73334 BP.
DE Chemically treated DNA repair gene fragment complementary to#64.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.8; DB 6; Length 73334;
Best Local Similarity 48.2%; Pred. No. 2.9e+02;
RESULT 1207
ID AAI96898 standard; cDNA; 733 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 2973.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 1.6%; Score 36.6; DB 4; Length 733;
Best Local Similarity 56.1%; Pred. No. 15;
RESULT 1208
ID AAK65390 standard; DNA; 1238 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20202.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 36.6; DB 4; Length 1238;
Best Local Similarity 55.0%; Pred. No. 22;
RESULT 1209
ID AAK70084 standard; DNA; 1238 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24896.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 36.6; DB 4; Length 1238;
Best Local Similarity 55.0%; Pred. No. 22;
RESULT 1210
ID ABN70650 standard; DNA; 1257 BP.
DE Streptococcus polynucleotide SEQ ID NO 9213.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 1.6%; Score 36.6; DB 6; Length 1257;
Best Local Similarity 47.9%; Pred. No. 22;
RESULT 1211
ID ACA50557 standard; DNA; 1260 BP.
DE Prokaryotic essential gene #32214.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

Query Match 1.6%; Score 36.6; DB 8; Length 1260;
Best Local Similarity 47.9%; Pred. No. 22;
RESULT 1212
ID ADE25650 standard; cDNA; 1830 BP.
DE Human cDNA differentially expressed in foam cells #54.
PN US2003194721-A1.
PD 16-OCT-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.6%; Score 36.6; DB 10; Length 1830;
Best Local Similarity 56.1%; Pred. No. 28;
RESULT 1213
ID ADN04923 standard; cDNA; 3400 BP.
DE Antipsoriatic cDNA sequence #676.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 36.6; DB 12; Length 3400;
Best Local Similarity 56.1%; Pred. No. 43;
RESULT 1214
ID ADF76479 standard; cDNA; 3401 BP.
DE Novel human secreted and transmembrane protein cDNA SeqID 153.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 36.6; DB 10; Length 3401;
Best Local Similarity 56.1%; Pred. No. 43;
RESULT 1215
ID ADK51974 standard; cDNA; 3401 BP.
DE Human atopic dermatitis/psoriasis-associated cDNA #7.
PN WO2004016785-A1.
PD 26-FEB-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTEENDO.
Query Match 1.6%; Score 36.6; DB 12; Length 3401;
Best Local Similarity 56.1%; Pred. No. 43;
RESULT 1216
ID ADR14492 standard; DNA; 3401 BP.
DE Human NF-kappaB pathway-associated gene SeqID493.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 1.6%; Score 36.6; DB 13; Length 3401;
Best Local Similarity 56.1%; Pred. No. 43;
RESULT 1217
ID ADP25120 standard; cDNA; 3401 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:2298.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 36.6; DB 13; Length 3401;
Best Local Similarity 56.1%; Pred. No. 43;
RESULT 1218
ID AAK77709 standard; DNA; 4028 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32521.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 1.6%; Score 36.6; DB 4; Length 4028;
Best Local Similarity 56.1%; Pred. No. 48;
RESULT 1219
ID ABX63656 standard; cDNA; 4040 BP.
DE Human cDNA #656 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Query Match 1.6%; Score 36.6; DB 8; Length 4040;
Best Local Similarity 56.1%; Pred. No. 48;
RESULT 1220
ID AAA70225 standard; DNA; 4056 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:358.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 1.6%; Score 36.6; DB 3; Length 4056;
Best Local Similarity 45.8%; Pred. No. 48;
RESULT 1221
ID AAS01528 standard; cDNA; 4541 BP.
DE Human secretory molecule cDNA sptm #18.
PN WO200123558-A2.
PD 05-APR-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.6%; Score 36.6; DB 4; Length 4541;
Best Local Similarity 55.6%; Pred. No. 52;
RESULT 1222
ID AAS01147 standard; DNA; 6233 BP.
DE Interferon induced nucleic acid, IFN2.
PN WO200118208-A2.
PD 15-MAR-2001.
PA (CURA-) CURAGEN CORP.
PA (BIOJ) BIOGEN INC.
Query Match 1.6%; Score 36.6; DB 4; Length 6233;
Best Local Similarity 56.1%; Pred. No. 64;
RESULT 1223
ID ABN89476 standard; cDNA; 19806 BP.
DE Human dehydrogenase genomic DNA SEQ ID NO:3.
PN WO200250255-A2.
PD 27-JUN-2002.
PA (PEKE) PE CORP NY.
Query Match 1.6%; Score 36.6; DB 6; Length 19806;
Best Local Similarity 51.5%; Pred. No. 1.4e+02;
RESULT 1224
ID ABD32550 standard; DNA; 37180 BP.
DE Mouse cancer-associated genomic DNA MD7-053.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.6%; Score 36.6; DB 13; Length 37180;
Best Local Similarity 51.5%; Pred. No. 2.1e+02;
RESULT 1225
Query Match 1.6%; Score 36.6; DB 13; Length 110000;
Best Local Similarity 43.5%; Pred. No. 4.3e+02;

RESULT 1226

ID ADJ43093 standard; cDNA; 585 BP.
DE Plant cDNA #4093.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.

Query Match 1.6%; Score 36.4; DB 12; Length 585;
Best Local Similarity 51.2%; Pred. No. 15;

RESULT 1227

ID ADJ43094 standard; cDNA; 718 BP.
DE Plant cDNA #4094.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.

Query Match 1.6%; Score 36.4; DB 12; Length 718;
Best Local Similarity 51.2%; Pred. No. 17;

RESULT 1228

ID ADJ41807 standard; cDNA; 761 BP.
DE Plant cDNA #2807.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.

Query Match 1.6%; Score 36.4; DB 12; Length 761;
Best Local Similarity 51.2%; Pred. No. 18;

RESULT 1229

ID ADJ41799 standard; cDNA; 864 BP.
DE Plant cDNA #2799.

PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ//) GLAZEBROOK J.
PA (GOFF//) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.

Query Match 1.6%; Score 36.4; DB 12; Length 864;
Best Local Similarity 53.5%; Pred. No. 20;

RESULT 1230

ID AAF57028 standard; cDNA; 1077 BP.
DE P. furiosus RFA polypeptide encoding cDNA.
PN WO200109347-A2.
PD 08-FEB-2001.
PA (STRA-) STRATAGENE.

Query Match 1.6%; Score 36.4; DB 4; Length 1077;
Best Local Similarity 53.5%; Pred. No. 23;

RESULT 1231

ID ACA10126 standard; cDNA; 1266 BP.
DE Human NOVX polynucleotide #16.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.

Query Match 1.6%; Score 36.4; DB 8; Length 1266;
Best Local Similarity 56.1%; Pred. No. 25;

RESULT 1232

ID ADE40267 standard; cDNA; 1266 BP.
DE Human NOV39b cDNA - SEQ ID 173.
PN WO2003064589-A2.
PD 07-AUG-2003.
PA (CURA-) CURAGEN CORP.

Query Match 1.6%; Score 36.4; DB 10; Length 1266;
Best Local Similarity 56.1%; Pred. No. 25;

RESULT 1233

ID ADO08284 standard; cDNA; 1266 BP.
DE Human NOVX polynucleotide #16.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSO BROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG//) BURGESS C E.
PA (CASM//) CASMAN S J.
PA (CHAP//) CHAPOVAL A.
PA (EDIN//) EDINGER S R.
PA (GERL//) GERLACH V.
PA (GORM//) GORMAN L.
PA (GUNT//) GUNTHER E.
PA (GUOX//) GUO X S.
PA (KEKU//) KEKUDA R.
PA (LEPL//) LEPLEY D M.

PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.

Query Match 1.6%; Score 36.4; DB 12; Length 1266;
Best Local Similarity 56.1%; Pred. No. 25;

RESULT 1234

ID ADC08349 standard; DNA; 2199 BP.
DE Rice DNA sequence Seq ID654 related to grain filling.
PN WO2003000905-A2.

PD 03-JAN-2003.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.6%; Score 36.4; DB 10; Length 2199;
Best Local Similarity 52.1%; Pred. No. 37;

RESULT 1235

ID AAC42784 standard; DNA; 2295 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36836.
PN EP1033405-A2.

PD 06-SEP-2000.

Query Match 1.6%; Score 36.4; DB 3; Length 2295;
Best Local Similarity 50.0%; Pred. No. 38;

RESULT 1236

ID AAC48369 standard; DNA; 2439 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 57229.
PN EP1033405-A2.

PD 06-SEP-2000.

Query Match 1.6%; Score 36.4; DB 3; Length 2439;
Best Local Similarity 50.0%; Pred. No. 39;

RESULT 1237

ID AAS45488 standard; DNA; 6620 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #97.
PN WO200168911-A2.

PD 20-SEP-2001.

PA (EPIG-) EPIGENOMICS AG.

Query Match 1.6%; Score 36.4; DB 4; Length 6620;
Best Local Similarity 51.4%; Pred. No. 76;

RESULT 1238

ID ABK28416 standard; DNA; 6620 BP.
DE DNA transcription associated complementary genomic DNA #145.
PN WO200192565-A2.

PD 06-DEC-2001.

PA (EPIG-) EPIGENOMICS AG.

Query Match 1.6%; Score 36.4; DB 6; Length 6620;
Best Local Similarity 51.4%; Pred. No. 76;

RESULT 1239

ID ABN80279 standard; DNA; 6620 BP.
DE Human chemically modified disease associated gene SEQ ID NO.296.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.4; DB 6; Length 6620;
Best Local Similarity 51.4%; Pred. No. 76;
RESULT 1240

ID ABL19228 standard; DNA; 10078 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 9157.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.6%; Score 36.4; DB 4; Length 10078;
Best Local Similarity 52.7%; Pred. No. 1e+02;
RESULT 1241

ID ABL33110 standard; DNA; 10957 BP.
DE Human immune system associated gene SEQ ID NO: 1083.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.4; DB 6; Length 10957;
Best Local Similarity 49.6%; Pred. No. 1.1e+02;
RESULT 1242

ID ABL33933 standard; DNA; 19734 BP.
DE Human immune system associated gene SEQ ID NO: 1906.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.4; DB 6; Length 19734;
Best Local Similarity 47.4%; Pred. No. 1.6e+02;
RESULT 1243

Query Match 1.6%; Score 36.4; DB 12; Length 110000;
Best Local Similarity 56.8%; Pred. No. 4.9e+02;
RESULT 1244

ID ABD33534 standard; DNA; 153995 BP.
DE Murine cancer-associated (CA) gene MD07-106.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.6%; Score 36.4; DB 13; Length 153995;
Best Local Similarity 50.0%; Pred. No. 6.1e+02;
RESULT 1245

ID ADL08119 standard; DNA; 158091 BP.
DE Human gene associated with low HDL-C LIPC #1.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 1.6%; Score 36.4; DB 12; Length 158091;
Best Local Similarity 51.9%; Pred. No. 6.2e+02;
RESULT 1246

ID ADS36450 standard; DNA; 321019 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1664.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 1.6%; Score 36.4; DB 13; Length 321019;

Best Local Similarity 49.5%; Pred. No. 9.8e+02;
RESULT 1247
ID ABD32707 standard; DNA; 329019 BP.
DE Human cancer-associated genomic DNA HD14-043.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.6%; Score 36.4; DB 13; Length 329019;
Best Local Similarity 49.5%; Pred. No. 9.9e+02;
RESULT 1248
ID ABQ65858 standard; DNA; 667 BP.
DE Arabidopsis thaliana polynucleotide SEQ ID NO 435.
PN US2002059663-A1.
PD 16-MAY-2002.
PA (GORL/) GORLACH J.
PA (ANYY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 1.6%; Score 36.2; DB 6; Length 667;
Best Local Similarity 52.3%; Pred. No. 19;
RESULT 1249
ID AAX20324 standard; DNA; 1300 BP.
DE Borrelia burgdorferi polynucleotide sequence #77.
PN WO9858943-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.
Query Match 1.6%; Score 36.2; DB 2; Length 1300;
Best Local Similarity 47.9%; Pred. No. 30;
RESULT 1250
ID ABL06636 standard; cDNA; 2878 BP..
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 14390.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.6%; Score 36.2; DB 4; Length 2878;
Best Local Similarity 44.1%; Pred. No. 50;
RESULT 1251
ID AAS51614 standard; DNA; 2988 BP.
DE Staphylococcus aureus DNA for cellular proliferation protein #31.
PN WO200170955-A2.
PD 27-SEP-2001.

PA (ELIT-) ELITRA PHARM INC.
Query Match 1.6%; Score 36.2; DB 4; Length 2988;
Best Local Similarity 47.2%; Pred. No. 52;
RESULT 1252
ID AAS54406 standard; DNA; 3030 BP.
DE Staphylococcus aureus DNA for cellular proliferation protein #718.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.6%; Score 36.2; DB 4; Length 3030;
Best Local Similarity 47.2%; Pred. No. 52;
RESULT 1253
ID AAA26288 standard; cDNA; 3129 BP.
DE Human secreted protein gene 8 SEQ ID NO:18.
PN WO200011014-A1.
PD 02-MAR-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 36.2; DB 3; Length 3129;
Best Local Similarity 49.0%; Pred. No. 53;
RESULT 1254
ID ABL17727 standard; DNA; 3507 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4654.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.6%; Score 36.2; DB 4; Length 3507;
Best Local Similarity 53.1%; Pred. No. 57;
RESULT 1255
ID ABL17726 standard; DNA; 5815 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4651.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.6%; Score 36.2; DB 4; Length 5815;
Best Local Similarity 53.1%; Pred. No. 80;
RESULT 1256
ID AAV58938 standard; DNA; 10095 BP.
DE Mycobacterium tuberculosis embCAB operon.
PN WO9841533-A1.
PD 24-SEP-1998.
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
Query Match 1.6%; Score 36.2; DB 2; Length 10095;
Best Local Similarity 51.6%; Pred. No. 1.2e+02;
RESULT 1257
ID ADJ12590 standard; DNA; 11122 BP.
DE DNA fragment of a BAC clone that encodes a human secreted protein Seq444.
PN US2004010132-A1.
PD 15-JAN-2004.
PA (ROSE//) ROSEN C A.
PA (BREW//) BREWER L A.
PA (DUAN//) DUAN R D.
PA (RUBE//) RUBEN S M.
PA (FLOR//) FLORENCE K A.
PA (GREE//) GREENE J M.
PA (YOUN//) YOUNG P E.
PA (FERR//) FERRIE A M.
PA (YUGG//) YU G.

PA (FLOR/) FLORENCE C.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H.
Query Match 1.6%; Score 36.2; DB 12; Length 11122;
Best Local Similarity 49.0%; Pred. No. 1.2e+02;
RESULT 1258
ID ADJ12540 standard; DNA; 11122 BP.
DE DNA fragment of a BAC clone that encodes a human secreted protein Seq394.
PN US2004010132-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (DUAN/) DUAN R D.
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (GREE/) GREENE J M.
PA (YOUN/) YOUNG P E.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (FLOR/) FLORENCE C.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H.
Query Match 1.6%; Score 36.2; DB 12; Length 11122;
Best Local Similarity 49.0%; Pred. No. 1.2e+02;
RESULT 1259
ID AAS29967 standard; DNA; 11172 BP.
DE Human lung antigen genomic DNA #37.
PN WO200155303-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 36.2; DB 5; Length 11172;
Best Local Similarity 50.9%; Pred. No. 1.2e+02;
RESULT 1260
ID ADB33304 standard; DNA; 11172 BP.
DE Human novel lung related polypeptide DNA SEQ ID NO 231.
PN US2003054368-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 36.2; DB 10; Length 11172;
Best Local Similarity 50.9%; Pred. No. 1.2e+02;
RESULT 1261
ID ABL32299 standard; DNA; 12507 BP.
DE Human immune system associated gene SEQ ID NO: 272.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.2; DB 6; Length 12507;
Best Local Similarity 49.2%; Pred. No. 1.3e+02;
RESULT 1262
ID ADD48574 standard; DNA; 28564 BP.
DE Human gene AL022727, SEQ ID NO 14280.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 1.6%; Score 36.2; DB 10; Length 28564;
Best Local Similarity 52.3%; Pred. No. 2.3e+02;

RESULT 1263

ID ADD46575 standard; DNA; 28564 BP.

DE Human gene AL022727, SEQ ID NO 12257.

PN WO2003016475-A2.

PD 27-FEB-2003.

PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

Query Match 1.6%; Score 36.2; DB 10; Length 28564;

Best Local Similarity 52.3%; Pred. No. 2.3e+02;

RESULT 1264

ID ABQ67006 standard; DNA; 33053 BP.

DE Human angiogenesis associated polynucleotide SEQ ID NO 36.

PN WO200246454-A2.

PD 13-JUN-2002.

PA (EPIG-) EPIGENOMICS AG.

Query Match 1.6%; Score 36.2; DB 6; Length 33053;

Best Local Similarity 46.0%; Pred. No. 2.5e+02;

RESULT 1265

ID AAD55116 standard; DNA; 98829 BP.

DE Human ACE reference DNA (GI 13027555).

PN WO2003020118-A2.

PD 13-MAR-2003.

PA (VITI-) VITIVITY INC.

Query Match 1.6%; Score 36.2; DB 9; Length 98829;

Best Local Similarity 50.9%; Pred. No. 5.3e+02;

RESULT 1266

Query Match 1.6%; Score 36.2; DB 4; Length 110000;

Best Local Similarity 51.6%; Pred. No. 5.6e+02;

RESULT 1267

Query Match 1.6%; Score 36.2; DB 4; Length 110000;

Best Local Similarity 51.6%; Pred. No. 5.6e+02;

RESULT 1268

ID ADH77123 standard; DNA; 126001 BP.

DE Human PAZ/PIWI domain-containing protein polynucleotide #3.

PN US2003232442-A1.

PD 18-DEC-2003.

PA (ISIS-) ISIS PHARM INC.

Query Match 1.6%; Score 36.2; DB 12; Length 126001;

Best Local Similarity 53.1%; Pred. No. 6.2e+02;

RESULT 1269

ID ADS69085 standard; cDNA; 279 BP.

DE Corn seedling-derived polynucleotide (cpds), SEQ ID 4101.

PN US2003237110-A9.

PD 25-DEC-2003.

PA (INCY-) INCYTE PHARM INC.

Query Match 1.6%; Score 36; DB 7; Length 279;

Best Local Similarity 51.6%; Pred. No. 12;

RESULT 1270

ID AAQ14776 standard; DNA; 303 BP.

DE IGF-I under alpha-S1-casein control regions.

PN EP451823-A.

PD 16-OCT-1991.

PA (CONE) CONSORTIUM ELEKTROCHEM IND.

Query Match 1.6%; Score 36; DB 2; Length 303;

Best Local Similarity 62.0%; Pred. No. 13;

RESULT 1271

ID ACH75803 standard; DNA; 527 BP.

DE Human genome derived single exon probe #8998.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 1.6%; Score 36; DB 12; Length 527;
Best Local Similarity 50.0%; Pred. No. 19;
RESULT 1272
ID AAA51052 standard; DNA; 719 BP.
DE Soybean SAMS promoter fragment.
PN WO200037662-A2.
PD 29-JUN-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 36; DB 3; Length 719;
Best Local Similarity 53.6%; Pred. No. 23;
RESULT 1273
ID ABD04376 standard; DNA; 801 BP.
DE Pseudomonas aeruginosa polynucleotide #2980.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.6%; Score 36; DB 11; Length 801;
Best Local Similarity 52.7%; Pred. No. 25;
RESULT 1274
ID ACA38703 standard; DNA; 1170 BP.
DE Prokaryotic essential gene #20360.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.6%; Score 36; DB 8; Length 1170;
Best Local Similarity 51.2%; Pred. No. 32;
RESULT 1275
ID ACA40348 standard; DNA; 1227 BP.
DE Prokaryotic essential gene #22005.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.6%; Score 36; DB 8; Length 1227;
Best Local Similarity 51.2%; Pred. No. 33;
RESULT 1276
ID AAA51042 standard; DNA; 1314 BP.
DE Soybean SAMS promoter region.
PN WO200037662-A2.
PD 29-JUN-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 36; DB 3; Length 1314;
Best Local Similarity 53.6%; Pred. No. 34;
RESULT 1277
ID ACA30500 standard; DNA; 1536 BP.
DE Prokaryotic essential gene #12157.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.6%; Score 36; DB 8; Length 1536;
Best Local Similarity 56.9%; Pred. No. 38;
RESULT 1278

ID AAA51051 standard; DNA; 1574 BP.
DE Soybean S-adenosyl-L-methionine synthetase promoter fragment.
PN WO200037662-A2.
PD 29-JUN-2000.
PA (DUP0) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 36; DB 3; Length 1574;
Best Local Similarity 53.6%; Pred. No. 39;
RESULT 1279
ID ABD04100 standard; DNA; 1785 BP.
DE Pseudomonas aeruginosa polynucleotide #2704.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.6%; Score 36; DB 11; Length 1785;
Best Local Similarity 52.7%; Pred. No. 42;
RESULT 1280
ID ABL41494 standard; cDNA; 1986 BP.
DE Human hypertension-related gene HRG-1 cDNA.
PN CN1181420-A.
PD 13-MAY-1998.
PA (UYBE-) UNIV BEIJING MEDICAL.
Query Match 1.6%; Score 36; DB 6; Length 1986;
Best Local Similarity 55.6%; Pred. No. 45;
RESULT 1281
ID AAA51050 standard; DNA; 2165 BP.
DE Soybean S-adenosyl-L-methionine synthetase promoter fragment.
PN WO200037662-A2.
PD 29-JUN-2000.
PA (DUP0) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 36; DB 3; Length 2165;
Best Local Similarity 53.6%; Pred. No. 48;
RESULT 1282
ID AAA51038 standard; DNA; 2336 BP.
DE Soybean S-adenosyl-L-methionine synthetase genomic DNA.
PN WO200037662-A2.
PD 29-JUN-2000.
PA (DUP0) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 36; DB 3; Length 2336;
Best Local Similarity 53.6%; Pred. No. 50;
RESULT 1283
ID AAA51055 standard; DNA; 3684 BP.
DE SAMS promoter::ATPS DNA fragment.
PN WO200037662-A2.
PD 29-JUN-2000.
PA (DUP0) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 36; DB 3; Length 3684;
Best Local Similarity 53.6%; Pred. No. 68;
RESULT 1284
ID AAA51056 standard; DNA; 3963 BP.
DE SAMS promoter::CGS1 DNA fragment.
PN WO200037662-A2.
PD 29-JUN-2000.
PA (DUP0) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 36; DB 3; Length 3963;
Best Local Similarity 53.6%; Pred. No. 72;
RESULT 1285
ID ADR20217 standard; DNA; 3979 BP.

DE Soybean expression cassette nucleotide sequence SEQ ID NO:90.
PN WO2004071467-A2.
PD 26-AUG-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 36; DB 13; Length 3979;
Best Local Similarity 53.6%; Pred. No. 72;
RESULT 1286
ID AAA51054 standard; DNA; 3985 BP.
DE SAMS promoter::GUS::3' Nos DNA fragment.
PN WO200037662-A2.
PD 29-JUN-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 36; DB 3; Length 3985;
Best Local Similarity 53.6%; Pred. No. 72;
RESULT 1287
ID AAC85792 standard; cDNA; 4550 BP.
DE hMfn2 cDNA.
PN WO200125274-A1.
PD 12-APR-2001.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 1.6%; Score 36; DB 4; Length 4550;
Best Local Similarity 55.6%; Pred. No. 78;
RESULT 1288
ID ABX96873 standard; DNA; 4550 BP.
DE DNA encoding the human mitofusin 2, Mfn2.
PN US2002168673-A1.
PD 14-NOV-2002.
PA (FULL/) FULLER M T.
PA (HALE/) HALE K G.
PA (SANT/) SANTEL A H.
Query Match 1.6%; Score 36; DB 8; Length 4550;
Best Local Similarity 55.6%; Pred. No. 78;
RESULT 1289
ID AAV69110 standard; DNA; 5064 BP.
DE Neisseria meningitidis ctrA-galE region genomic DNA.
PN WO9845312-A1.
PD 15-OCT-1998.
PA (UYEM-) UNIV EMORY.
Query Match 1.6%; Score 36; DB 2; Length 5064;
Best Local Similarity 46.4%; Pred. No. 84;
RESULT 1290
ID ABL33976 standard; DNA; 8456 BP.
DE Human immune system associated gene SEQ ID NO: 1949.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36; DB 6; Length 8456;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
RESULT 1291
ID ABQ66990 standard; DNA; 9118 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 20.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36; DB 6; Length 9118;
Best Local Similarity 48.5%; Pred. No. 1.2e+02;
RESULT 1292

ID ABN80049 standard; DNA; 9543 BP.
DE Human chemically modified disease associated gene SEQ ID NO 66.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.6%; Score 36; DB 6; Length 9543;
 Best Local Similarity 48.5%; Pred. No. 1.3e+02;
RESULT 1293

ID ABL32976 standard; DNA; 18512 BP.
DE Human immune system associated gene SEQ ID NO: 949.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.6%; Score 36; DB 6; Length 18512;
 Best Local Similarity 50.0%; Pred. No. 2e+02;
RESULT 1294

 Query Match 1.6%; Score 36; DB 13; Length 89736;
 Best Local Similarity 49.5%; Pred. No. 5.7e+02;
RESULT 1295

ID ABD32711 standard; DNA; 94781 BP.
DE Mouse cancer-associated genomic DNA MD14-044.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 1.6%; Score 36; DB 13; Length 94781;
 Best Local Similarity 52.7%; Pred. No. 5.9e+02;
RESULT 1296

 Query Match 1.6%; Score 36; DB 4; Length 110000;
 Best Local Similarity 51.2%; Pred. No. 6.5e+02;
RESULT 1297

 Query Match 1.6%; Score 36; DB 4; Length 110000;
 Best Local Similarity 51.2%; Pred. No. 6.5e+02;
RESULT 1298

ID AAV86185 standard; cDNA; 600 BP.
DE EST clone J635.
PN WO9845435-A2.
PD 15-OCT-1998.
PA (GEMY) GENETICS INST INC.
 Query Match 1.5%; Score 35.8; DB 2; Length 600;
 Best Local Similarity 17.4%; Pred. No. 23;
RESULT 1299

ID ADC92334 standard; DNA; 831 BP.
DE E. faecium DNA sequence SEQ ID 1961.
PN US6583275-B1.
PD 24-JUN-2003.
PA ...(GENO-) GENOME THERAPEUTICS CORP.
 Query Match 1.5%; Score 35.8; DB 10; Length 831;
 Best Local Similarity 53.1%; Pred. No. 29;
RESULT 1300

ID ABL25777 standard; DNA; 1395 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28804.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
 Query Match 1.5%; Score 35.8; DB 4; Length 1395;
 Best Local Similarity 55.1%; Pred. No. 41;
RESULT 1301

ID AAQ74684 standard; cDNA; 1650 BP.
DE Early Ripening Tomato protein ERT1b gene.
PN WO9421794-A1.
PD 29-SEP-1994.
PA (ZENE) ZENECA LTD.
Query Match 1.5%; Score 35.8; DB 2; Length 1650;
Best Local Similarity 52.3%; Pred. No. 46;
RESULT 1302
ID ACA30586 standard; DNA; 1899 BP.
DE Prokaryotic essential gene #12243.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.5%; Score 35.8; DB 8; Length 1899;
Best Local Similarity 49.7%; Pred. No. 50;
RESULT 1303
ID ABL25776 standard; DNA; 3894 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28801.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.5%; Score 35.8; DB 4; Length 3894;
Best Local Similarity 55.1%; Pred. No. 81;
RESULT 1304
ID ABK31378 standard; DNA; 5338 BP.
DE Signal transduction associated gene modified DNA #111.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.8; DB 6; Length 5338;
Best Local Similarity 48.7%; Pred. No. 1e+02;
RESULT 1305
ID ABL70329 standard; DNA; 5338 BP.
DE Chemically treated cell signalling DNA sequence#110.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.8; DB 6; Length 5338;
Best Local Similarity 48.7%; Pred. No. 1e+02;
RESULT 1306
ID AAS61280 standard; DNA; 5338 BP.
DE Human gene regulation-associated gene oligonucleotide #235.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.8; DB 6; Length 5338;
Best Local Similarity 48.7%; Pred. No. 1e+02;
RESULT 1307
ID ABL33491 standard; DNA; 8392 BP.
DE Human immune system associated gene SEQ ID NO: 1464.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.8; DB 6; Length 8392;
Best Local Similarity 47.8%; Pred. No. 1.4e+02;
RESULT 1308
ID ABL32795 standard; DNA; 8951 BP.

DE Human immune system associated gene SEQ ID NO: 768.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.8; DB 6; Length 8951;
Best Local Similarity 55.1%; Pred. No. 1.4e+02;
RESULT 1309
ID AAK75286 standard; DNA; 10055 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30098.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 35.8; DB 4; Length 10055;
Best Local Similarity 48.3%; Pred. No. 1.5e+02;
RESULT 1310
ID AAS45328 standard; DNA; 11735 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #17.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.8; DB 4; Length 11735;
Best Local Similarity 46.6%; Pred. No. 1.7e+02;
RESULT 1311
ID ABK28167 standard; DNA; 11735 BP.
DE DNA transcription associated genomic DNA #21.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.8; DB 6; Length 11735;
Best Local Similarity 46.6%; Pred. No. 1.7e+02;
RESULT 1312
ID AAS61141 standard; DNA; 11735 BP.
DE Human gene regulation-associated gene oligonucleotide #96.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.8; DB 6; Length 11735;
Best Local Similarity 46.6%; Pred. No. 1.7e+02;
RESULT 1313
ID AAK65368 standard; DNA; 18564 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20180.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 35.8; DB 4; Length 18564;
Best Local Similarity 56.3%; Pred. No. 2.3e+02;
RESULT 1314
ID ABZ74461 standard; DNA; 18564 BP.
DE Secreted protein gene 300 genomic fragment HSQDO85, SEQ ID NO:1608.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 35.8; DB 8; Length 18564;
Best Local Similarity 56.3%; Pred. No. 2.3e+02;
RESULT 1315
ID ADA98881 standard; DNA; 18564 BP.
DE Human secreted protein-related DNA sequence #474.

PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 35.8; DB 8; Length 18564;
 Best Local Similarity 56.3%; Pred. No. 2.3e+02;
RESULT 1316
ID AAK75287 standard; DNA; 18855 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30099.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 35.8; DB 4; Length 18855;
 Best Local Similarity 48.3%; Pred. No. 2.3e+02;
RESULT 1317
 Query Match 1.5%; Score 35.8; DB 13; Length 110000;
 Best Local Similarity 50.3%; Pred. No. 7.4e+02;
RESULT 1318
ID ADQ80254 standard; cDNA; 127145 BP.
DE Hermansky-Pudlak syndrome associated cDNA.
PN WO2004063709-A2.
PD 29-JUL-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 1.5%; Score 35.8; DB 13; Length 127145;
 Best Local Similarity 56.3%; Pred. No. 8.1e+02;
RESULT 1319
ID ABX43735 standard; cDNA; 219 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #8900.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
 Query Match 1.5%; Score 35.6; DB 8; Length 219;
 Best Local Similarity 54.6%; Pred. No. 14;
RESULT 1320
ID ACN59359 standard; cDNA; 584 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-030-Q6-K6-E4, SEQ:14140.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
 Query Match 1.5%; Score 35.6; DB 13; Length 584;
 Best Local Similarity 52.7%; Pred. No. 26;
RESULT 1321
ID ADS56832 standard; cDNA; 2008 BP.
DE Bacterial polynucleotide #8819.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
 Query Match 1.5%; Score 35.6; DB 13; Length 2008;

Best Local Similarity 49.5%; Pred. No. 60;
RESULT 1322
ID ADS47566 standard; cDNA; 2109 BP.
DE Bacterial polynucleotide #2309.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 1.5%; Score 35.6; DB 13; Length 2109;
Best Local Similarity 45.6%; Pred. No. 62;
RESULT 1323
ID AAZ93713 standard; DNA; 2112 BP..
DE F-box protein Pop2 coding sequence.
PN WO200022110-A2.
PD 20-APR-2000.
PA (HARD) HARVARD COLLEGE.
Query Match 1.5%; Score 35.6; DB 3; Length 2112;
Best Local Similarity 45.6%; Pred. No. 62;
RESULT 1324
ID AAT84152 standard; DNA; 2314 BP.
DE DNA encoding a Staphylococcus aureus protein of unknown function.
PN WO9730070-A1.
PD 21-AUG-1997.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 1.5%; Score 35.6; DB 2; Length 2314;
Best Local Similarity 47.6%; Pred. No. 66;
RESULT 1325
ID ADS56393 standard; cDNA; 2856 BP.
DE Bacterial polynucleotide #8380.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 1.5%; Score 35.6; DB 13; Length 2856;
Best Local Similarity 51.2%; Pred. No. 76;
RESULT 1326
ID ABL32945 standard; DNA; 5234 BP.
DE Human immune system associated gene SEQ ID NO: 918.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.6; DB 6; Length 5234;
Best Local Similarity 52.7%; Pred. No. 1.1e+02;
RESULT 1327
ID ABL32776 standard; DNA; 6782 BP.
DE Human immune system associated gene SEQ ID NO: 749.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.6; DB 6; Length 6782;
Best Local Similarity 51.2%; Pred. No. 1.3e+02;

RESULT 1328

ID AAX20267 standard; DNA; 6810 BP.
DE Borrelia burgdorferi polynucleotide sequence #20.
PN WO9858943-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.

Query Match 1.5%; Score 35.6; DB 2; Length 6810;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;

RESULT 1329

ID ABN80082 standard; DNA; 10250 BP.
DE Human chemically modified disease associated gene SEQ ID NO 99.
PN WO200200927-A2.
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.

Query Match 1.5%; Score 35.6; DB 6; Length 10250;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;

RESULT 1330

ID ABL92221 standard; DNA; 11049 BP.
DE Chemically treated DNA repair gene fragment complementary to#15.
PN WO200181622-A2.
PD 01-NOV-2001.

PA (EPIG-) EPIGENOMICS AG.

Query Match 1.5%; Score 35.6; DB 6; Length 11049;
Best Local Similarity 51.9%; Pred. No. 1.9e+02;

RESULT 1331

ID ABL49324 standard; DNA; 11049 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 24.
PN WO200177377-A2.
PD 18-OCT-2001.

PA (EPIG-) EPIGENOMICS AG.

Query Match 1.5%; Score 35.6; DB 6; Length 11049;
Best Local Similarity 51.9%; Pred. No. 1.9e+02;

RESULT 1332

ID AAS45501 standard; DNA; 11812 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #103.
PN WO200168911-A2.
PD 20-SEP-2001.

PA (EPIG-) EPIGENOMICS AG.

Query Match 1.5%; Score 35.6; DB 4; Length 11812;
Best Local Similarity 49.5%; Pred. No. 1.9e+02;

RESULT 1333

ID AAS46741 standard; DNA; 11812 BP.
DE Tumour suppressor gene derived chemically modified sequence #465.
PN WO200168912-A2.
PD 20-SEP-2001.

PA (EPIG-) EPIGENOMICS AG.

Query Match 1.5%; Score 35.6; DB 4; Length 11812;
Best Local Similarity 49.5%; Pred. No. 1.9e+02;

RESULT 1334

ID ABL34118 standard; DNA; 11812 BP.
DE Human immune system associated gene SEQ ID NO: 2091.
PN WO200200928-A2.
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.

Query Match 1.5%; Score 35.6; DB 6; Length 11812;
Best Local Similarity 49.5%; Pred. No. 1.9e+02;

RESULT 1335

ID ABK28431 standard; DNA; 11812 BP.
DE DNA transcription associated genomic DNA #153.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.5%; Score 35.6; DB 6; Length 11812;
Best Local Similarity 49.5%; Pred. No. 1.9e+02;

RESULT 1336

ID ABL32571 standard; DNA; 18997 BP.
DE Human immune system associated gene SEQ ID NO: 544.
PN WO200200928-A2.
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.

Query Match 1.5%; Score 35.6; DB 6; Length 18997;
Best Local Similarity 49.2%; Pred. No. 2.7e+02;

RESULT 1337

ID ABK33949 standard; DNA; 18997 BP.
DE Human DNA for staging of Astrocytomas, complement, #16.
PN WO200202808-A2.
PD 10-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.

Query Match 1.5%; Score 35.6; DB 6; Length 18997;
Best Local Similarity 49.2%; Pred. No. 2.7e+02;

RESULT 1338

ID ADA20353 standard; DNA; 18997 BP.
DE Prostate tumour related genomic DNA complement sample #9.
PN WO2002103042-A2.
PD 27-DEC-2002.

PA (EPIG-) EPIGENOMICS AG.

Query Match 1.5%; Score 35.6; DB 8; Length 18997;
Best Local Similarity 49.2%; Pred. No. 2.7e+02;

RESULT 1339

ID ADA84160 standard; DNA; 18997 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:18.
PN WO2002103041-A2.
PD 27-DEC-2002.

PA (EPIG-) EPIGENOMICS AG.

Query Match 1.5%; Score 35.6; DB 8; Length 18997;
Best Local Similarity 49.2%; Pred. No. 2.7e+02;

RESULT 1340

Query Match 1.5%; Score 35.6; DB 2; Length 110000;
Best Local Similarity 55.7%; Pred. No. 8.5e+02;

RESULT 1341

ID ADS69964 standard; cDNA; 262 BP.
DE Corn seedling-derived polynucleotide (cpds), SEQ ID 4980.
PN US2003237110-A9.
PD 25-DEC-2003.

PA (INCY-) INCYTE PHARM INC.

Query Match 1.5%; Score 35.4; DB 7; Length 262;
Best Local Similarity 53.2%; Pred. No. 18;

RESULT 1342

ID ABN65577 standard; cDNA; 556 BP.
DE Human cancer related polynucleotide SEQ ID NO 5544.
PN WO200214500-A2.
PD 21-FEB-2002.

PA (CHIR) CHIRON CORP.

PA (HYSE-) HYSEQ INC.
Query Match 1.5%; Score 35.4; DB 6; Length 556;
Best Local Similarity 53.2%; Pred. No. 29;
RESULT 1343
ID AAK88255 standard; cDNA; 612 BP.
DE Human digestive system antigen coding sequence SEQ ID NO: 571.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 35.4; DB 4; Length 612;
Best Local Similarity 52.9%; Pred. No. 31;
RESULT 1344
ID AAS39407 standard; cDNA; 612 BP.
DE cDNA encoding novel human colon associated polypeptide #60.
PN WO200155302-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 35.4; DB 5; Length 612;
Best Local Similarity 52.9%; Pred. No. 31;
RESULT 1345
ID ADB32133 standard; cDNA; 612 BP.
DE Human novel colon related polypeptide cDNA SEQ ID NO 70.
PN US2003050231-A1.
PD 13-MAR-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 1.5%; Score 35.4; DB 9; Length 612;
Best Local Similarity 52.9%; Pred. No. 31;
RESULT 1346
ID AAH34792 standard; cDNA; 707 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1874.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 35.4; DB 4; Length 707;
Best Local Similarity 49.78%; Pred. No. 34;
RESULT 1347
ID ADJ43568 standard; cDNA; 824 BP.
DE Plant cDNA #4568.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 1.5%; Score 35.4; DB 12; Length 824;
Best Local Similarity 53.2%; Pred. No. 38;
RESULT 1348
ID ADB52352 standard; DNA; 864 BP.

DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:2894.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 1.5%; Score 35.4; DB 10; Length 864;
Best Local Similarity 52.3%; Pred. No. 39;
RESULT 1349
ID ABK73608 standard; DNA; 1140 BP.
DE Bacillus licheniformis genomic sequence tag (GST) #899.
PN WO200229113-A2.
PD 11-APR-2002.
PA (NOVO) NOVOZYMES BIOTECH INC.
PA (NOVO) NOVOZYMES AS.
Query Match 1.5%; Score 35.4; DB 6; Length 1140;
Best Local Similarity 47.5%; Pred. No. 47;
RESULT 1350
ID AAC36917 standard; DNA; 1203 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 15522.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.5%; Score 35.4; DB 3; Length 1203;
Best Local Similarity 54.1%; Pred. No. 49;
RESULT 1351
ID ABD16646 standard; DNA; 1272 BP.
DE Pseudomonas aeruginosa polynucleotide #15250.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.5%; Score 35.4; DB 11; Length 1272;
Best Local Similarity 52.3%; Pred. No. 51;
RESULT 1352
ID ABZ13055 standard; DNA; 1455 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 860.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.5%; Score 35.4; DB 6; Length 1455;
Best Local Similarity 52.3%; Pred. No. 56;
RESULT 1353
ID ADC25954 standard; DNA; 1455 BP.
DE Thale cress UDP-glucosyltransferase DNA.
PN WO2003066836-A2.
PD 14-AUG-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.5%; Score 35.4; DB 10; Length 1455;
Best Local Similarity 52.3%; Pred. No. 56;
RESULT 1354
ID AAD13657 standard; DNA; 1473 BP.
DE Arabidopsis thaliana glucosyltransferase (GTase) A41 gene.
PN WO200159140-A1.
PD 16-AUG-2001.
PA (UYYO-) UNIV YORK.
Query Match 1.5%; Score 35.4; DB 4; Length 1473;
Best Local Similarity 52.3%; Pred. No. 56;
RESULT 1355
ID ADJ40246 standard; cDNA; 1479 BP.

DE Plant cDNA #1246.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 1.5%; Score 35.4; DB 12; Length 1479;
Best Local Similarity 53.2%; Pred. No. 56;
RESULT 1356
ID ADA71336 standard; DNA; 1490 BP.
DE Rice gene, SEQ ID 4659.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.5%; Score 35.4; DB 8; Length 1490;
Best Local Similarity 45.7%; Pred. No. 56;
RESULT 1357
ID AAC42466 standard; DNA; 1516 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 35666.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.5%; Score 35.4; DB 3; Length 1516;
Best Local Similarity 52.3%; Pred. No. 57;
RESULT 1358
ID ABD16834 standard; DNA; 1614 BP.
DE Pseudomonas aeruginosa polynucleotide #15438.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.5%; Score 35.4; DB 11; Length 1614;
Best Local Similarity 52.3%; Pred. No. 60;
RESULT 1359
ID AAC47594 standard; DNA; 1669 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 54396.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.5%; Score 35.4; DB 3; Length 1669;
Best Local Similarity 54.1%; Pred. No. 61;
RESULT 1360
ID ABA99470 standard; cDNA; 1715 BP.
DE B. napus SGT1 cDNA.
PN WO200206320-A2.
PD 24-JAN-2002.
PA (PFLA-) INST PFLANZENBIOCHEMIE.
Query Match 1.5%; Score 35.4; DB 6; Length 1715;
Best Local Similarity 52.3%; Pred. No. 62;
RESULT 1361
ID AAC47078 standard; DNA; 1759 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52482.

PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.5%; Score 35.4; DB 3; Length 1759;
Best Local Similarity 54.1%; Pred. No. 63;
RESULT 1362
ID ADA71684 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5009.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.5%; Score 35.4; DB 8; Length 2000;
Best Local Similarity 48.7%; Pred. No. 69;
RESULT 1363
ID ADO36063 standard; DNA; 2902 BP.
DE Novel mouse gene sequence #736.
PN WO2004046310-A2.
PD 03-JUN-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 1.5%; Score 35.4; DB 12; Length 2902;
Best Local Similarity 56.4%; Pred. No. 88;
RESULT 1364
ID ABL08782 standard; cDNA; 5059 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 20828.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.5%; Score 35.4; DB 4; Length 5059;
Best Local Similarity 46.5%; Pred. No. 1.3e+02;
RESULT 1365
ID AAS46721 standard; DNA; 5995 BP.
DE Tumour suppressor gene derived chemically modified sequence #444.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.4; DB 4; Length 5995;
Best Local Similarity 48.7%; Pred. No. 1.4e+02;
RESULT 1366
ID AAX13432 standard; DNA; 6645 BP.
DE Enterococcus faecalis genome contig SEQ ID NO:495.
PN WO9850555-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 35.4; DB 2; Length 6645;
Best Local Similarity 49.2%; Pred. No. 1.5e+02;
RESULT 1367
ID ABS99227 standard; DNA; 6645 BP.
DE Enterococcus faecalis contig sequence #495.
PN US2002120116-A1.
PD 29-AUG-2002.
PA (KUNS/) KUNSCH C A.
PA (DILL/) DILLON P J.
PA (BARA/) BARASH S.
Query Match 1.5%; Score 35.4; DB 6; Length 6645;
Best Local Similarity 49.2%; Pred. No. 1.5e+02;
RESULT 1368
ID ABL33929 standard; DNA; 6801 BP.
DE Human immune system associated gene SEQ ID NO: 1902.

PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.4; DB 6; Length 6801;
Best Local Similarity 46.8%; Pred. No. 1.5e+02;
RESULT 1369
ID ABL92291 standard; DNA; 6801 BP.
DE Chemically treated DNA repair gene fragment complementary to#50.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.4; DB 6; Length 6801;
Best Local Similarity 46.8%; Pred. No. 1.5e+02;
RESULT 1370
ID ABL49362 standard; DNA; 6801 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 62.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.4; DB 6; Length 6801;
Best Local Similarity 46.8%; Pred. No. 1.5e+02;
RESULT 1371
ID ABL33637 standard; DNA; 7306 BP.
DE Human immune system associated gene SEQ ID NO: 1610.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.4; DB 6; Length 7306;
Best Local Similarity 45.5%; Pred. No. 1.6e+02;
RESULT 1372
ID AAI99335 standard; DNA; 7408 BP.
DE Human excretory related polynucleotide SEQ ID NO 1099.
PN WO200155313-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 35.4; DB 4; Length 7408;
Best Local Similarity 55.2%; Pred. No. 1.6e+02;
RESULT 1373
ID AAI63685 standard; DNA; 7408 BP.
DE Human kidney related polynucleotide SEQ ID NO 1000.
PN WO200155323-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 35.4; DB 5; Length 7408;
Best Local Similarity 55.2%; Pred. No. 1.6e+02;
RESULT 1374
ID ABK31382 standard; DNA; 7459 BP.
DE Signal transduction associated gene modified DNA #113.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.4; DB 6; Length 7459;
Best Local Similarity 46.0%; Pred. No. 1.6e+02;
RESULT 1375
ID ABL92304 standard; DNA; 13919 BP.
DE Chemically treated DNA repair gene fragment#57.
PN WO200181622-A2.

PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.4; DB 6; Length 13919;
Best Local Similarity 51.6%; Pred. No. 2.5e+02;
RESULT 1376
ID ABL32654 standard; DNA; 17211 BP.
DE Human immune system associated gene SEQ ID NO: 627.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.4; DB 6; Length 17211;
Best Local Similarity 49.2%; Pred. No. 2.9e+02;
RESULT 1377
ID AAK67051 standard; DNA; 30626 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21863.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 35.4; DB 4; Length 30626;
Best Local Similarity 49.2%; Pred. No. 4.2e+02;
RESULT 1378
ID ACN45192 standard; DNA; 82660 BP.
DE Mouse genomic sequence mCG9397.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.5%; Score 35.4; DB 11; Length 82660;
Best Local Similarity 55.2%; Pred. No. 8.1e+02;
RESULT 1379
ID ADB12769 standard; DNA; 139308 BP.
DE Human PRKR DNA.
PN DE10128838-A1.
PD 02-JAN-2003.
PA (GENP-) GENPROFILE AG.
Query Match 1.5%; Score 35.4; DB 8; Length 139308;
Best Local Similarity 55.2%; Pred. No. 1.1e+03;
RESULT 1380
ID AAC10087 standard; cDNA; 274 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 14162.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 1.5%; Score 35.2; DB 3; Length 274;
Best Local Similarity 59.8%; Pred. No. 21;
RESULT 1381
ID ADL43834 standard; DNA; 461 BP.
DE Human ovarian cancer DNA marker #17724.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 35.2; DB 5; Length 461;
Best Local Similarity 51.4%; Pred. No. 30;
RESULT 1382
ID ACH78507 standard; DNA; 507 BP.
DE Human genome derived single exon probe #11702.
PN US2003194704-A1.
PD 16-OCT-2003.

PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 1.5%; Score 35.2; DB 12; Length 507;
Best Local Similarity 52.8%; Pred. No. 32;
RESULT 1383
ID ADR60605 standard; cDNA; 639 BP.
DE Cotton cDNA sequence, SEQ ID 1386.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match 1.5%; Score 35.2; DB 13; Length 639;
Best Local Similarity 52.0%; Pred. No. 37;
RESULT 1384
ID ABN69110 standard; DNA; 786 BP.
DE Streptococcus polynucleotide SEQ ID NO 6133.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 1.5%; Score 35.2; DB 6; Length 786;
Best Local Similarity 52.8%; Pred. No. 42;
RESULT 1385
ID ABN98454 standard; DNA; 1011 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 222.
PN US2002023281-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANYY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 1.5%; Score 35.2; DB 6; Length 1011;
Best Local Similarity 50.3%; Pred. No. 50;
RESULT 1386
ID ACH92210 standard; DNA; 1101 BP.
DE Human genome derived single exon probe #25405.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.

PA (HANZ/) HANZEL D K.
Query Match 1.5%; Score 35.2; DB 12; Length 1101;
Best Local Similarity 52.8%; Pred. No. 53;
RESULT 1387
ID ABZ42066 standard; cDNA; 1473 BP.
DE Arabidopsis thaliana gene #50 modulated by PTGS.
PN WO200281695-A2.
PD 17-OCT-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (FRIE-) FRIEDRICH MIESCHER INST.
Query Match 1.5%; Score 35.2; DB 8; Length 1473;
Best Local Similarity 48.5%; Pred. No. 64;
RESULT 1388
ID AAV16721 standard; cDNA to mRNA; 1506 BP.
DE Nucleic acid encoding rat Neural-Wiskott-Aldrich syndrome protein.
PN JP10072494-A.
PD 17-MAR-1998.
PA (MITS-) MITSUI SEIYAKU KOGYO KK.
PA (TAKE/) TAKENAWA T.
Query Match 1.5%; Score 35.2; DB 2; Length 1506;
Best Local Similarity 52.0%; Pred. No. 65;
RESULT 1389
ID AAH77907 standard; DNA; 1588 BP.
DE Nucleotide sequence of a rat N-WASP protein.
PN WO200144292-A2.
PD 21-JUN-2001.
PA (CNRS) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
Query Match 1.5%; Score 35.2; DB 4; Length 1588;
Best Local Similarity 52.0%; Pred. No. 68;
RESULT 1390
ID ABZ16116 standard; DNA; 2000 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 3921.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.5%; Score 35.2; DB 6; Length 2000;
Best Local Similarity 49.0%; Pred. No. 79;
RESULT 1391
ID ABT42528 standard; DNA; 2049 BP.
DE Human nucleic acid-associated protein (NAAP) coding sequence #9.
PN WO2003010329-A2.
PD 06-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.5%; Score 35.2; DB 8; Length 2049; ..
Best Local Similarity 52.8%; Pred. No. 80;
RESULT 1392
ID ADC30266 standard; cDNA; 2069 BP.
DE Human novel cDNA sequence, SEQ ID NO:348.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 1.5%; Score 35.2; DB 10; Length 2069;
Best Local Similarity 52.8%; Pred. No. 81;
RESULT 1393
ID ADF03150 standard; DNA; 2208 BP.

DE Bacterial polynucleotide #3435.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.5%; Score 35.2; DB 10; Length 2208;
Best Local Similarity 49.0%; Pred. No. 84;
RESULT 1394
ID ADM02604 standard; cDNA; 2241 BP.
DE Human cDNA of the invention SEQ ID NO:1289.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 1.5%; Score 35.2; DB 11; Length 2241;
Best Local Similarity 52.8%; Pred. No. 85;
RESULT 1395
ID ADM02673 standard; cDNA; 2525 BP.
DE Human cDNA of the invention SEQ ID NO:1358.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 1.5%; Score 35.2; DB 11; Length 2525;
Best Local Similarity 52.8%; Pred. No. 92;
RESULT 1396
ID ABZ32269 standard; DNA; 2625 BP.
DE Candida albicans essential gene SEQ ID NO 6556.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.5%; Score 35.2; DB 6; Length 2625;
Best Local Similarity 52.0%; Pred. No. 94;
RESULT 1397
ID ADS89352 standard; DNA; 3862 BP.
DE Oligonucleotide of the invention SEQ ID NO:368.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.2; DB 13; Length 3862;
Best Local Similarity 49.0%; Pred. No. 1.2e+02;
RESULT 1398
ID ABK40013 standard; DNA; 5244 BP.
DE Human chemically pretreated gene sequence #48 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.2; DB 6; Length 5244;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
RESULT 1399
ID ABL32828 standard; DNA; 6009 BP.
DE Human immune system associated gene SEQ ID NO: 801.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.2; DB 6; Length 6009;
Best Local Similarity 52.0%; Pred. No. 1.6e+02;
RESULT 1400
ID ABK31371 standard; DNA; 6012 BP.
DE Signal transduction associated gene modified complementary DNA #107.

PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 6; Length 6012;
 Best Local Similarity 48.5%; Pred. No. 1.6e+02;
RESULT 1401
ID ABL70328 standard; DNA; 6012 BP.
DE Chemically treated cell signalling DNA sequence complementary to#109.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 6; Length 6012;
 Best Local Similarity 48.5%; Pred. No. 1.6e+02;
RESULT 1402
ID AAS61275 standard; DNA; 6012 BP.
DE Human gene regulation-associated gene oligonucleotide #230.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 6; Length 6012;
 Best Local Similarity 48.5%; Pred. No. 1.6e+02;
RESULT 1403
ID AAS46300 standard; DNA; 6862 BP.
DE Tumour suppressor gene derived chemically modified sequence #22.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 4; Length 6862;
 Best Local Similarity 49.0%; Pred. No. 1.8e+02;
RESULT 1404
ID ABL32223 standard; DNA; 6862 BP.
DE Human immune system associated gene SEQ ID NO: 196.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 6; Length 6862;
 Best Local Similarity 49.0%; Pred. No. 1.8e+02;
RESULT 1405
ID AAS61082 standard; DNA; 6862 BP.
DE Human gene regulation-associated gene oligonucleotide #37.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 6; Length 6862;
 Best Local Similarity 49.0%; Pred. No. 1.8e+02;
RESULT 1406
ID ABN80083 standard; DNA; 10250 BP.
DE Human chemically modified disease associated gene SEQ ID NO 100.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 6; Length 10250;
 Best Local Similarity 52.0%; Pred. No. 2.3e+02;
RESULT 1407
ID ABL34179 standard; DNA; 13084 BP.
DE Human immune system associated gene SEQ ID NO: 2152.
PN WO200200928-A2.

PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.2; DB 6; Length 13084;
Best Local Similarity 54.7%; Pred. No. 2.7e+02;
RESULT 1408
ID ABL33344 standard; DNA; 17674 BP.
DE Human immune system associated gene SEQ ID NO: 1317.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.2; DB 6; Length 17674;
Best Local Similarity 52.0%; Pred. No. 3.3e+02;
RESULT 1409
ID ADA02885 standard; DNA; 96593 BP.
DE Mouse Blm carcinoma associated gene, SEQ ID NO:1403.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.5%; Score 35.2; DB 9; Length 96593;
Best Local Similarity 53.7%; Pred. No. 1e+03;
RESULT 1410
ID ADB72623 standard; DNA; 96593 BP.
DE Mouse Blm gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.5%; Score 35.2; DB 10; Length 96593;
Best Local Similarity 53.7%; Pred. No. 1e+03;
RESULT 1411
ID ADM74480 standard; DNA; 96593 BP.
DE Murine carcinoma associated (CA) nucleic acid #76.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 1.5%; Score 35.2; DB 12; Length 96593;
Best Local Similarity 53.7%; Pred. No. 1e+03;
RESULT 1412
ID ADC85364 standard; DNA; 96594 BP.
DE Human Pap coding sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.5%; Score 35.2; DB 10; Length 96594;
Best Local Similarity 53.7%; Pred. No. 1e+03;
RESULT 1413
ID ACN43994 standard; DNA; 109586 BP.
DE Human genomic sequence hCG23847.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.5%; Score 35.2; DB 11; Length 109586;
Best Local Similarity 45.8%; Pred. No. 1.1e+03;
RESULT 1414
ID AAT42063 standard; DNA; 1830121 BP.
DE Haemophilus influenzae complete genome sequence.
PN WO9633276-A1.

PD 24-OCT-1996.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 1.5%; Score 35.2; DB 2; Length 110000;
Best Local Similarity 47.0%; Pred. No. 1.1e+03;
RESULT 1415
Query Match 1.5%; Score 35.2; DB 5; Length 110000;
Best Local Similarity 50.9%; Pred. No. 1.1e+03;
RESULT 1416
Query Match 1.5%; Score 35.2; DB 6; Length 110000;
Best Local Similarity 52.8%; Pred. No. 1.1e+03;
RESULT 1417
ID ABD32827 standard; DNA; 129381 BP.
DE Human cancer-associated genomic DNA HD17-008.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.5%; Score 35.2; DB 13; Length 129381;
Best Local Similarity 50.6%; Pred. No. 1.2e+03;
RESULT 1418
ID AAK74668 standard; DNA; 340 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29480.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 35; DB 4; Length 340;
Best Local Similarity 49.2%; Pred. No. 28;
RESULT 1419
ID AAK74669 standard; DNA; 340 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29481.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 35; DB 4; Length 340;
Best Local Similarity 49.2%; Pred. No. 28;
RESULT 1420
ID AAF62609 standard; DNA; 1413 BP.
DE R. serpentina arbutin synthase DNA.
PN WO200107631-A2.
PD 01-FEB-2001.
PA (HENK) HENKEL KGAA.
Query Match 1.5%; Score 35; DB 4; Length 1413;
Best Local Similarity 54.2%; Pred. No. 72;
RESULT 1421
ID AAD13665 standard; DNA; 1425 BP.
DE ...Arabidopsis thaliana glucosyltransferase (GTase) A962 gene.
PN WO200159140-A1.
PD 16-AUG-2001.
PA (UYYO-) UNIV YORK.
Query Match 1.5%; Score 35; DB 4; Length 1425;
Best Local Similarity 52.4%; Pred. No. 72;
RESULT 1422
ID ABZ14807 standard; DNA; 1425 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2612.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.5%; Score 35; DB 6; Length 1425;
Best Local Similarity 52.4%; Pred. No. 72;
RESULT 1423
ID ADA70022 standard; DNA; 1485 BP.
DE Rice gene, SEQ ID 3345.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.5%; Score 35; DB 8; Length 1485;
Best Local Similarity 50.9%; Pred. No. 74;
RESULT 1424
ID ADJ39593 standard; cDNA; 1485 BP.
DE Plant cDNA #593.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 1.5%; Score 35; DB 12; Length 1485;
Best Local Similarity 50.9%; Pred. No. 74;
RESULT 1425
ID ACA22042 standard; DNA; 3277 BP.
DE Prokaryotic essential gene #3699.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.5%; Score 35; DB 8; Length 3277;
Best Local Similarity 59.6%; Pred. No. 1.3e+02;
RESULT 1426
ID ACA21975 standard; DNA; 4217 BP.
DE Prokaryotic essential gene #3632.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.5%; Score 35; DB 8; Length 4217;
Best Local Similarity 59.6%; Pred. No. 1.5e+02;
RESULT 1427
ID ABL33906 standard; DNA; 4415 BP.
DE Human immune system associated gene SEQ ID NO: 1879.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35; DB 6; Length 4415;
Best Local Similarity 47.9%; Pred. No. 1.5e+02;
RESULT 1428
ID ABL34602 standard; DNA; 4415 BP.
DE Human metastasis associated gene SEQ ID NO: 155.
PN WO200177376-A2.

PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35; DB 6; Length 4415;
Best Local Similarity 47.9%; Pred. No. 1.5e+02;
RESULT 1429
ID ABL70423 standard; DNA; 4415 BP.
DE Chemically treated cell signalling DNA sequence#157.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35; DB 6; Length 4415;
Best Local Similarity 47.9%; Pred. No. 1.5e+02;
RESULT 1430
ID ADS99863 standard; DNA; 4415 BP.
DE Bisulphite treated human gene associated with metastasis #78.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 1.5%; Score 35; DB 7; Length 4415;
Best Local Similarity 47.9%; Pred. No. 1.5e+02;
RESULT 1431
ID ADS48728 standard; cDNA; 4566 BP.
DE Bacterial polynucleotide #3471.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 1.5%; Score 35; DB 13; Length 4566;
Best Local Similarity 50.3%; Pred. No. 1.6e+02;
RESULT 1432
ID ADQ23570 standard; DNA; 4944 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6390.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 1.5%; Score 35; DB 12; Length 4944;
Best Local Similarity 55.3%; Pred. No. 1.6e+02;
RESULT 1433
ID AAQ80911 standard; cDNA; 5181 BP.
DE Plasmodium falciparum MSA-1 gene cDNA.
PN WO9428930-A1.
PD 22-DEC-1994.
PA (VIRO-) VIROGENETICS CORP.
Query Match 1.5%; Score 35; DB 2; Length 5181;
Best Local Similarity 55.3%; Pred. No. 1.7e+02;
RESULT 1434
ID ABD32852 standard; cDNA; 5895 BP.
DE Mouse cancer-associated cDNA MR17-032.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.5%; Score 35; DB 13; Length 5895;

Best Local Similarity 51.6%; Pred. No. 1.9e+02;
RESULT 1435
ID ADP76048 standard; DNA; 5935 BP.
DE DNA of mouse epidermal growth factor receptor, SEQ ID No 23.
PN WO2004055055-A1.
PD 01-JUL-2004.
PA (LICN) LICENTIA LTD.
Query Match 1.5%; Score 35; DB 13; Length 5935;
Best Local Similarity 51.6%; Pred. No. 1.9e+02;
RESULT 1436
ID AAA81730 standard; DNA; 9133 BP.
DE N. meningitidis partial DNA sequence gnm_277 SEQ ID NO:277.
PN WO200022430-A2.
PD 20-APR-2000.
PA (CHIR) CHIRON CORP.
Query Match 1.5%; Score 35; DB 3; Length 9133;
Best Local Similarity 55.3%; Pred. No. 2.5e+02;
RESULT 1437
ID ABL70189 standard; DNA; 15282 BP.
DE Chemically treated cell signalling DNA sequence#40.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35; DB 6; Length 15282;
Best Local Similarity 49.7%; Pred. No. 3.5e+02;
RESULT 1438
ID AAS61139 standard; DNA; 15282 BP.
DE Human gene regulation-associated gene oligonucleotide #94.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35; DB 6; Length 15282;
Best Local Similarity 49.7%; Pred. No. 3.5e+02;
RESULT 1439
ID ABL33415 standard; DNA; 17389 BP.
DE Human immune system associated gene SEQ ID NO: 1388.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35; DB 6; Length 17389;
Best Local Similarity 49.7%; Pred. No. 3.8e+02;
RESULT 1440
ID ACN43954 standard; DNA; 95683 BP.
DE Human genomic sequence hCG37570.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.5%; Score 35; DB 11; Length 95683;
Best Local Similarity 53.2%; Pred. No. 1.2e+03;
RESULT 1441
Query Match 1.5%; Score 35; DB 3; Length 110000;
Best Local Similarity 55.3%; Pred. No. 1.3e+03;
RESULT 1442
Query Match 1.5%; Score 35; DB 12; Length 110000;
Best Local Similarity 47.5%; Pred. No. 1.3e+03;
RESULT 1443
ID ADQ97319 standard; DNA; 117829 BP.

DE Human cancer associated sequence HD08-031, SEQ ID 296.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.5%; Score 35; DB 12; Length 117829;
Best Local Similarity 45.7%; Pred. No. 1.3e+03;
RESULT 1444
ID ABQ88126 standard; cDNA; 159400 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 33.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 1.5%; Score 35; DB 6; Length 159400;
Best Local Similarity 53.2%; Pred. No. 1.6e+03;
RESULT 1445
ID ABD32851 standard; DNA; 181413 BP.
DE Mouse cancer-associated genomic DNA MD17-032.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.5%; Score 35; DB 13; Length 181413;
Best Local Similarity 51.6%; Pred. No. 1.8e+03;
RESULT 1446
ID AAF21608 standard; DNA; 349980 BP.
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.
PN WO200066791-A1.
PD 09-NOV-2000.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 1.5%; Score 35; DB 3; Length 349980;
Best Local Similarity 55.3%; Pred. No. 2.6e+03;
RESULT 1447
ID ABX38043 standard; cDNA; 413 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3208.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 34.8; DB 8; Length 413;
Best Local Similarity 52.8%; Pred. No. 36;
RESULT 1448
ID ACN49798 standard; cDNA; 495 BP.
DE Cotton primed seed EST Clone ID: LIB3825-031-Q6-N6-A10, SEQ:4579.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 34.8; DB 13; Length 495;
Best Local Similarity 50.6%; Pred. No. 41;
RESULT 1449
ID ACA05131 standard; cDNA; 531 BP.
DE Rice leaf expression sequence label #44.

PN CN1367260-A.
PD 04-SEP-2002.
PA (UYZH-) UNIV ZHEJIANG.
Query Match 1.5%; Score 34.8; DB 8; Length 531;
Best Local Similarity 60.6%; Pred. No. 43;
RESULT 1450
ID ADJ43307 standard; cDNA; 615 BP.
DE Plant cDNA #4307.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 1.5%; Score 34.8; DB 12; Length 615;
Best Local Similarity 52.8%; Pred. No. 47;
RESULT 1451
ID ADK59885 standard; DNA; 624 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #7268.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 1.5%; Score 34.8; DB 10; Length 624;
Best Local Similarity 56.8%; Pred. No. 48;
RESULT 1452
ID ABZ12278 standard; DNA; 1158 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 83.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.5%; Score 34.8; DB 6; Length 1158;
Best Local Similarity 51.3%; Pred. No. 72;
RESULT 1453
ID ABL29557 standard; DNA; 1200 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 40144.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.5%; Score 34.8; DB 4; Length 1200;
Best Local Similarity 55.9%; Pred. No. 74;
RESULT 1454
ID ABZ66714 standard; DNA; 1329 BP.
DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 90.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 1.5%; Score 34.8; DB 10; Length 1329;
Best Local Similarity 50.6%; Pred. No. 79;

RESULT 1455

ID ACA29043 standard; DNA; 1386 BP.
DE Prokaryotic essential gene #10700.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.5%; Score 34.8; DB 8; Length 1386;
Best Local Similarity 45.3%; Pred. No. 81;

RESULT 1456

ID ADF89822 standard; DNA; 1726 BP.
DE Triterpene saponin pathway associated nucleotide sequence, SEQ ID 30.
PN WO2003093425-A2.
PD 13-NOV-2003.
PA (ROBE-) ROBERTS NOBLE FOUND INC SAMMUEL.
Query Match 1.5%; Score 34.8; DB 10; Length 1726;
Best Local Similarity 45.3%; Pred. No. 94;

RESULT 1457

ID ACA31023 standard; DNA; 2001 BP.
DE Prokaryotic essential gene #12680.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.5%; Score 34.8; DB 8; Length 2001;
Best Local Similarity 50.6%; Pred. No. 1e+02;

RESULT 1458

ID ABL30171 standard; DNA; 2350 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41986.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.5%; Score 34.8; DB 4; Length 2350;
Best Local Similarity 52.0%; Pred. No. 1.2e+02;

RESULT 1459

ID ABN84912 standard; cDNA; 2846 BP.
DE AMP-binding enzyme family 33217 cDNA.
PN WO200259284-A2.
PD 01-AUG-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 34.8; DB 6; Length 2846;
Best Local Similarity 31.5%; Pred. No. 1.3e+02;

RESULT 1460

ID ADL14183 standard; cDNA; 2846 BP.
DE Novel human gene 33217 cDNA.
PN US2004058355-A1.
PD 25-MAR-2004.
PA (MILL-), MILLENNIUM PHARM INC.
Query Match 1.5%; Score 34.8; DB 12; Length 2846;
Best Local Similarity 31.5%; Pred. No. 1.3e+02;

RESULT 1461

ID ABD32853 standard; cDNA; 2986 BP.
DE Mouse cancer-associated cDNA MR17-032.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.5%; Score 34.8; DB 13; Length 2986;
Best Local Similarity 48.9%; Pred. No. 1.4e+02;

RESULT 1462

ID ABL29556 standard; DNA; 3323 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 40141.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.5%; Score 34.8; DB 4; Length 3323;
Best Local Similarity 55.9%; Pred. No. 1.5e+02;
RESULT 1463

ID ABL50557 standard; DNA; 3446 BP.
DE Micromonospora carbonacea everninomicin locus nucleotide contig 3.
PN WO200155180-A2.
PD 02-AUG-2001.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
PA (FARN/) FARNET C.
Query Match 1.5%; Score 34.8; DB 4; Length 3446;
Best Local Similarity 50.6%; Pred. No. 1.5e+02;
RESULT 1464

ID ABL26186 standard; DNA; 3957 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 30031.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.5%; Score 34.8; DB 4; Length 3957;
Best Local Similarity 52.0%; Pred. No. 1.6e+02;
RESULT 1465

ID AAT86702 standard; DNA; 6263 BP.
DE DNA encoding thermostable esterase E009.
PN WO9725058-A1.
PD 17-JUL-1997.
PA (THER-) THERMOGEN INC.
Query Match 1.5%; Score 34.8; DB 2; Length 6263;
Best Local Similarity 50.6%; Pred. No. 2.2e+02;
RESULT 1466

ID AAS03396 standard; DNA; 6263 BP.
DE Thermus DNA encoding a partial thermostable esterase, E009.
PN US6218163-B1.
PD 17-APR-2001.
PA (THER-) THERMOGEN INC.
Query Match 1.5%; Score 34.8; DB 4; Length 6263;
Best Local Similarity 50.6%; Pred. No. 2.2e+02;
RESULT 1467

ID AAX08523 standard; DNA; 6265 BP.
DE NBP46 (root lectin) genomic DNA.
PN WO9907223-A1.
PD 18-FEB-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 1.5%; Score 34.8; DB 2; Length 6265;
Best Local Similarity 47.7%; Pred. No. 2.2e+02;
RESULT 1468

ID AAS46760 standard; DNA; 7900 BP.
DE Tumour suppressor gene derived chemically modified sequence #484.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 34.8; DB 4; Length 7900;
Best Local Similarity 45.6%; Pred. No. 2.6e+02;
RESULT 1469

ID ABL19298 standard; DNA; 8005 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 9367.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
 Query Match 1.5%; Score 34.8; DB 4; Length 8005;
 Best Local Similarity 55.9%; Pred. No. 2.6e+02;
RESULT 1470

ID ABK39954 standard; DNA; 8076 BP.
DE Human chemically pretreated gene sequence #18 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 34.8; DB 6; Length 8076;
 Best Local Similarity 48.9%; Pred. No. 2.6e+02;
RESULT 1471

ID ABL30170 standard; DNA; 9716 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41983.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
 Query Match 1.5%; Score 34.8; DB 4; Length 9716;
 Best Local Similarity 52.0%; Pred. No. 3e+02;
RESULT 1472

ID ABL33467 standard; DNA; 10606 BP.
DE Human immune system associated gene SEQ ID NO: 1440.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 34.8; DB 6; Length 10606;
 Best Local Similarity 52.0%; Pred. No. 3.1e+02;
RESULT 1473

ID AAS45314 standard; DNA; 11260 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #10.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 34.8; DB 4; Length 11260;
 Best Local Similarity 49.5%; Pred. No. 3.3e+02;
RESULT 1474

ID ABK28153 standard; DNA; 11260 BP.
DE DNA transcription associated genomic DNA #14.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 34.8; DB 6; Length 11260;
 Best Local Similarity 49.5%; Pred. No. 3.3e+02;
RESULT 1475

ID ABN80038 standard; DNA; 11260 BP.
DE Human chemically modified disease associated gene SEQ ID NO 55.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 34.8; DB 6; Length 11260;
 Best Local Similarity 49.5%; Pred. No. 3.3e+02;
RESULT 1476

ID AAA96368 standard; DNA; 12117 BP.

DE Polymorphic repeat microsatellite sequences present in the CTLA4 locus.
PN WO200056856-A2.
PD 28-SEP-2000.
PA (GEMY) GENETICS INST INC.
Query Match 1.5%; Score 34.8; DB 3; Length 12117;
Best Local Similarity 57.3%; Pred. No. 3.4e+02;
RESULT 1477
ID ABL32729 standard; DNA; 14307 BP.
DE Human immune system associated gene SEQ ID NO: 702.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 34.8; DB 6; Length 14307;
Best Local Similarity 50.0%; Pred. No. 3.8e+02;
RESULT 1478
ID ABL32631 standard; DNA; 14987 BP.
DE Human immune system associated gene SEQ ID NO: 604.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 34.8; DB 6; Length 14987;
Best Local Similarity 44.3%; Pred. No. 3.9e+02;
RESULT 1479
ID ABN80238 standard; DNA; 15121 BP.
DE Human chemically modified disease associated gene SEQ ID NO 255.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 34.8; DB 6; Length 15121;
Best Local Similarity 47.0%; Pred. No. 4e+02;
RESULT 1480
ID ABL32362 standard; DNA; 15674 BP.
DE Human immune system associated gene SEQ ID NO: 335.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 34.8; DB 6; Length 15674;
Best Local Similarity 43.9%; Pred. No. 4.1e+02;
RESULT 1481
ID ABL34476 standard; DNA; 15674 BP.
DE Human metastasis associated gene SEQ ID NO: 29.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 34.8; DB 6; Length 15674;
Best Local Similarity 43.9%; Pred. No. 4.1e+02;
RESULT 1482
ID ABL70513 standard; DNA; 15674 BP.
DE Chemically treated cell signalling DNA sequence#202.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 34.8; DB 6; Length 15674;
Best Local Similarity 43.9%; Pred. No. 4.1e+02;
RESULT 1483
ID ADS99737 standard; DNA; 15674 BP.
DE Bisulphite treated human gene associated with metastasis #15.

PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 1.5%; Score 34.8; DB 7; Length 15674;
Best Local Similarity 43.9%; Pred. No. 4.1e+02;
RESULT 1484
ID ABL32191 standard; DNA; 17137 BP.
DE Human immune system associated gene SEQ ID NO: 164.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 34.8; DB 6; Length 17137;
Best Local Similarity 47.3%; Pred. No. 4.3e+02;
RESULT 1485
ID ACN43972 standard; DNA; 47601 BP.
DE Mouse genomic sequence mCG12024.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.5%; Score 34.8; DB 11; Length 47601;
Best Local Similarity 50.0%; Pred. No. 8.5e+02;
RESULT 1486
ID ABZ66811 standard; DNA; 48221 BP.
DE Orthosomycin biosynthetic gene cluster SEQ ID NO 280.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 1.5%; Score 34.8; DB 10; Length 48221;
Best Local Similarity 50.6%; Pred. No. 8.6e+02;
RESULT 1487
Query Match 1.5%; Score 34.8; DB 10; Length 110000;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
RESULT 1488
ID ADL13649 standard; DNA; 127098 BP.
DE Osteoarthritis-associated polymorphic nucleotide #181.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.5%; Score 34.8; DB 10; Length 127098;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
RESULT 1489
ID ABD32851 standard; DNA; 181413 BP.
DE Mouse cancer-associated genomic DNA MD17-032.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.5%; Score 34.8; DB 13; Length 181413;
Best Local Similarity 48.9%; Pred. No. 2e+03;
RESULT 1490
ID ADQ97421 standard; DNA; 228835 BP.
DE Human cancer associated sequence HD08-046, SEQ ID 398.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.5%; Score 34.8; DB 12; Length 228835;

Best Local Similarity 53.7%; Pred. No. 2.3e+03;
RESULT 1491
ID ABX49902 standard; cDNA; 317 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #15067.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 34.6; DB 8; Length 317;
Best Local Similarity 50.6%; Pred. No. 35;
RESULT 1492
ID ABX49371 standard; cDNA; 320 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #14536.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 34.6; DB 8; Length 320;
Best Local Similarity 52.4%; Pred. No. 35;
RESULT 1493
ID ACN59310 standard; cDNA; 416 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-029-Q6-N6-B6, SEQ:14091.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 34.6; DB 13; Length 416;
Best Local Similarity 53.7%; Pred. No. 42;
RESULT 1494
ID ADC93274 standard; DNA; 528 BP.
DE E. faecium DNA sequence SEQ ID 2901.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.5%; Score 34.6; DB 10; Length 528;
Best Local Similarity 58.1%; Pred. No. 49;
RESULT 1495
ID ACN56850 standard; cDNA; 637 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-011-Q6-K6-E2, SEQ:11631.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 34.6; DB 13; Length 637;
Best Local Similarity 51.6%; Pred. No. 56;
RESULT 1496
ID ABZ32076 standard; DNA; 645 BP.
DE Candida albicans essential gene SEQ ID NO 6363.
PN WO200253728-A2.

PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.5%; Score 34.6; DB 6; Length 645;
Best Local Similarity 44.8%; Pred. No. 56;
RESULT 1497
ID ADR60325 standard; cDNA; 646 BP.
DE Cotton cDNA sequence, SEQ ID 1106.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match 1.5%; Score 34.6; DB 13; Length 646;
Best Local Similarity 53.7%; Pred. No. 56;
RESULT 1498
ID AAS52930 standard; DNA; 771 BP.
DE Enterococcus faecalis DNA for cellular proliferation protein #358.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.5%; Score 34.6; DB 4; Length 771;
Best Local Similarity 51.6%; Pred. No. 63;
RESULT 1499
ID ABT42401 standard; DNA; 1008 BP.
DE Toxicity modelling related rat gene SEQ ID No 2103.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 1.5%; Score 34.6; DB 10; Length 1008;
Best Local Similarity 54.3%; Pred. No. 75;
RESULT 1500
ID ADP72800 standard; DNA; 1008 BP.
DE Renal toxin progression gene marker #1389.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 1.5%; Score 34.6; DB 12; Length 1008;
Best Local Similarity 54.3%; Pred. No. 75;

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OM nucleic - nucleic search, using sw model

Run on: February 15, 2005, 06:28:57 ; Search time 407 Seconds
(without alignments)
9327.179 Million cell updates/sec

Title: US-10-017-867A-281

Perfect score: 2320

Sequence: 1 agggtcccttagccgggcgc.....tctctcccaacctcactaa 2320

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
	No.	Score	Match	Length	DB ID	
1	1147.8	49.5	2426	4	US-09-774-528-26	Sequence 26, Appl
2	143.2	6.2	2966	4	US-09-976-594-241	Sequence 241, App
3	137	5.9	1629	4	US-09-949-016-2596	Sequence 2596, Ap
4	137	5.9	1708	4	US-09-949-016-2595	Sequence 2595, Ap
5	136.4	5.9	2107	3	US-09-180-852-1	Sequence 1, Appli
6	136	5.9	1832	4	US-09-949-016-2734	Sequence 2734, Ap
7	136	5.9	1854	4	US-09-356-806-39	Sequence 39, Appl
8	131.6	5.7	2092	4	US-09-356-806-7	Sequence 7, Appli
9	130	5.6	2092	4	US-09-949-016-2594	Sequence 2594, Ap
10	130	5.6	2092	4	US-09-949-016-3181	Sequence 3181, Ap
11	128.4	5.5	1976	4	US-09-356-806-112	Sequence 112, App

12	127.6	5.5	1413	3	US-09-813-918-1	Sequence 1, Appli	
13	127.6	5.5	1413	4	US-10-060-311-1	Sequence 1, Appli	
14	125.2	5.4	2093	4	US-09-949-016-1128	Sequence 1128, Ap	
15	119.6	5.2	2351	4	US-09-949-016-76	Sequence 76, Appl	
16	119.6	5.2	2351	4	US-09-949-016-1813	Sequence 1813, Ap	
17	118	5.1	2336	5	PCT-US92-00282-1	Sequence 1, Appli	
18	115.4	5.0	1323	4	US-09-949-016-2735	Sequence 2735, Ap	
19	115.4	5.0	1323	4	US-09-949-016-2736	Sequence 2736, Ap	
20	111.2	4.8	2339	5	PCT-US92-00282-2	Sequence 2, Appli	
21	95.6	4.1	735	4	US-09-305-856B-17	Sequence 17, Appli	
22	79.2	3.4	7218	1	US-08-232-463-14	Sequence 14, Appli	
23	68.2	2.9	769	4	US-09-270-767-2063	Sequence 2063, Ap	
24	68.2	2.9	769	4	US-09-270-767-17345	Sequence 17345, A	
c	25	64.6	2.8	1369	4	US-09-270-767-13787	Sequence 13787, A
	26	63.8	2.8	689	4	US-09-356-806-5	Sequence 5, Appli
	27	63.8	2.8	19732	4	US-09-949-016-12870	Sequence 12870, A
	28	63.8	2.8	19732	4	US-09-949-016-14923	Sequence 14923, A
	29	63.8	2.8	19733	4	US-09-949-016-14336	Sequence 14336, A
	30	62.4	2.7	391	3	US-09-370-838-21	Sequence 21, Appli
	31	62.4	2.7	391	4	US-09-854-133-21	Sequence 21, Appli
	32	62.2	2.7	1591	4	US-09-356-806-44	Sequence 44, Appli
	33	62.2	2.7	20441	4	US-09-949-016-14476	Sequence 14476, A
	34	59	2.5	18373	4	US-09-949-016-14338	Sequence 14338, A
	35	59	2.5	18452	4	US-09-949-016-14337	Sequence 14337, A
c	36	57.4	2.5	831	4	US-09-270-767-29825	Sequence 29825, A
	37	56.8	2.4	1731	2	US-08-466-583-1	Sequence 1, Appli
	38	56.8	2.4	1731	4	US-08-265-427-1	Sequence 1, Appli
	39	56.8	2.4	1731	5	PCT-US95-07820-1	Sequence 1, Appli
	40	56.2	2.4	513	4	US-09-270-767-14001	Sequence 14001, A
	41	56.2	2.4	983	4	US-09-671-317-386	Sequence 386, App
	42	55.8	2.4	350	4	US-09-513-999C-3284	Sequence 3284, Ap
	43	55	2.4	1602	4	US-09-356-806-117	Sequence 117, App
	44	55	2.4	20599	4	US-09-949-016-14477	Sequence 14477, A
	45	55	2.4	20599	4	US-09-949-016-14478	Sequence 14478, A
	46	53.4	2.3	783	5	PCT-US92-00282-22	Sequence 22, Appli
	47	53.4	2.3	17020	4	US-09-949-016-11818	Sequence 11818, A
	48	53.4	2.3	17021	4	US-09-949-016-13555	Sequence 13555, A
	49	49.2	2.1	657	4	US-09-669-751-104	Sequence 104, App
	50	48.8	2.1	1141	4	US-09-806-708B-22	Sequence 22, Appli
	51	48.6	2.1	1001	4	US-09-671-317-404	Sequence 404, App
c	52	46	2.0	41737	4	US-09-949-016-12204	Sequence 12204, A
c	53	46	2.0	41741	4	US-09-949-016-16983	Sequence 16983, A
	54	44.6	1.9	762	3	US-09-615-192A-218	Sequence 218, App
c	55	44.6	1.9	1141	4	US-09-806-708B-22	Sequence 22, Appli
	56	43.6	1.9	1001	4	US-09-671-317-413	Sequence 413, App
	57	43.6	1.9	1001	4	US-09-671-317-414	Sequence 414, App
	58	43.6	1.9	1001	4	US-09-671-317-415	Sequence 415, App
	59	43.6	1.9	1001	4	US-09-671-317-417	Sequence 417, App
	60	43.6	1.9	1021	4	US-09-356-806-115	Sequence 115, App
	61	43.2	1.9	1001	4	US-09-671-317-416	Sequence 416, App
	62	42.6	1.8	2025	3	US-08-942-012B-23	Sequence 23, Appli
	63	42	1.8	408	4	US-09-270-767-1461	Sequence 1461, Ap
	64	42	1.8	408	4	US-09-270-767-16743	Sequence 16743, A
	65	42	1.8	1800	6	5180581-1	Patent No. 5180581
	66	42	1.8	1800	6	5180581-1	Patent No. 5180581
	67	42	1.8	2793	1	US-08-281-916-5	Sequence 5, Appli
	68	42	1.8	2793	2	US-08-460-725-7	Sequence 7, Appli

Qy	458	ATGGATTCTTAAAGAATGAGAACCTCGACATGGTATGTTGAAACTTTGACTACTGT	517
Db	1	ATGGACTTCTTAAAAATGAGAACCTTGACCTAGTACTTCTGATTCAATGGATCTGT	60
Qy	518	CCTTCCTGATTGCTGAGAAGCTGGAGGCCATTGTGCCATTCTTCACATTC	577
Db	61	TCTTGTCTAATTGTTGAAAAGCTGGAAACGATTGTGTCCTTCTTCCTTCATTT	120
Qy	578	GGCTCTTGGATTGGCTACCAA---TCCCCTGTCTTATGTTCCAGTATTCCGTTCC	634
Db	121	AGCTATATGGACTTGGTTACCAAGCGCCCCCTGTCCTATGCTCCAGTGTATGGTTCT	180
Qy	635	TTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTCTGATGTTCTTAGT	694
Db	181	GGTCTAACTGACCAATGGACTTCTGGGGCCGAGTGAAGAACTTCTGATGTTCTGAT	240
Qy	695	TTCTGCAGGAGGCAACAGCACATGCAGTCTACATTGACAACACCATCAAGGAACATTTC	754
Db	241	TTCTCCATGAAGCAAAGGGAAATCCTTCTCAGTATGACAGCACTATCCAGGAGCATT	300
Qy	755	ACAGAAGGCTCTAGGCCAGTTGTCTCATCTCTACTGAAAGCAGAGTTGTTCTCATT	814
Db	301	GTGGAAGGCTCTCAGCCAGTGTGTCGACCTCTACTGAAAGCTGAGCTGTTGTC	360
Qy	815	AACTCTGACTTTGCCTTGATTTGCTCGACCTCTGCTTCCAAACACTGTTATGTTGGA	874
Db	361	AACTCTGACTTTGCTTGATTTGCTCGTCCCTGTTCCAAACACAGTCTATGTTGGA	420
Qy	875	GGCTTGATGGAAAAACCTATTAAACCACTGACCAAGACTGGAGAACATTGTCAGAAC	934
Db	421	GGTTTACTGGACAAACCTGTTCAAGCCAAACAGACTGGAGAACATTGTCAGAAC	480
Qy	935	TTTGGGGACTCTGGTTTGTCTGACCTTGGCTCCATGGTAACACCTGTCAGAAC	994
Db	481	TTTGGAGACTCAGGTTGTCTGTGGCCCTGGCTCTATAGTGAGCATGATTGTCAG	540
Qy	995	CCGGAAATCTCAAGGAGATGAACAATGCCTTGCTCACCTACCCCAAGGGGTGATATGG	1054
Db	541	AAGGAAATTATTAAGGAGATGAACAGTGCCCTTGCTCACCTCCCTCAAGGGGTGCTATGG	600
Qy	1055	AAGTGTCACTGTTCTCATTGGCCAAAGATGTCCACCTGGCTGCAAATGTGAAATTGTG	1114
Db	601	ACATGTAAGACTTCTCATTGGCCAAAGATGTCACTTGGCCCCAAATGTCAAATCATG	660
Qy	1115	GAATGGCTTCCCTCAGAGTGACCTCTGGCTCACCAAGCATCCGCTGTTGTCA	1174
Db	661	GATTGGCTTCCACAGACTGACCTCTAGCTCACCTAGCATTGCTGTTGTCAC	720
Qy	1175	GGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCATGGTGGGATCCCT	1234
Db	721	GGAGGGATGAACAGTGTGATGGAGGGCTGTCCATCATGGAGTACCCATGGTGGGATTCCA	780
Qy	1235	CTCTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCAGGAAAGTTGGTCTTCT	1294
Db	781	TTTTTTTGTACCAACCTGAAAACATGGTCCGAGTAGAAGCAGGAAACCTGGTCTTCT	840

Qy	1295	ATTCAGTTAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAA	1354
Db	841	ATTCAGCTACAGACGCTCAAGGCAGAGTCATTGCGCTCACCATGAAAAAAATCATAGAA	900
Qy	1355	GACAAGAGATAACAAGTCCGGCAGTGGCTGCCAGTGTCTGCCTGCCACCCGCTC	1414
Db	901	GACAAGAGGTACAAGTCTGCAGCAATGGCCTCCAAGATTATCAGGCACTCCCACCCACTG	960
Qy	1415	AGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCCAGACAGGGGGCGCGACG	1474
Db	961	ACCCCTGCCAGAGGCTTTGGGCTGGATAGATCATATCTTGCAGACAGGGGTGCAGCA	1020
Qy	1475	CACCTCAAGCCCTATGTCTTCAGCAGCCCTGGCATGAGCAGTACCTGTTGCACGTTT	1534
Db	1021	CATCTCAAGCCATATGCTTCCAGCAGCCATGGCATGAGCAGTACATGCTTGATGTCTTC	1080
Qy	1535	GTGTTCTGCTGGGCTCACTCTGGGACTCTATGGCTTGTTGTGGGAAGCTGCTGGCATG	1594
Db	1081	CTCTTCTCCTAGGGCTCATGCTGGTACTTGTGGCTTAGTGTAAAGGTTCTGTTGCT	1140
Qy	1595	GCTGTCTGGTGGCTGCGTGGGCCAGAAAGGTGAAGGAGACATAA	1639
Db	1141	GTAACCAGGTATCTGAGTATAGCAACGAAGGTCAAGGAGGCATAA	1185

RESULT 8

AK041045

LOCUS AK041045 1353 bp mRNA linear HTC 03-APR-2004
 DEFINITION Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530069C13 product:hypothetical UDP-glucuronosyl and UDP-glucosyl transferase containing protein, full insert sequence.
 ACCESSION AK041045
 VERSION AK041045.1 GI:26334156
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 1353)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL:<http://genome.gsc.riken.jp/>, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL:<http://genome.gsc.riken.jp/>
 URL:<http://fantom.gsc.riken.jp/>.

FEATURES Location/Qualifiers

source

- 1. .1353
- /organism="Mus musculus"
- /mol_type="mRNA"
- /strain="C57BL/6J"
- /db_xref="FANTOM_DB:A530069C13"
- /db_xref="taxon:10090"
- /clone="A530069C13"

/sex="male"
 /tissue_type="aorta and vein"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="adult"
 83. .991
 /note="unnamed protein product; hypothetical
 UDP-glucuronosyl and UDP-glucosyl transferase containing
 protein (InterPro|IPR002213, evidence: InterPro)
 putative"
 /codon_start=1
 /protein_id="BAC30796.1"
 /db_xref="GI:26334157"
 /translation="MAAHRRLMSFLFLEVILLEAAKILTISTLSASHYIVISRVSQ
 VLHEGGHNVTKLLYESANIPDFRKEKPSYQVINWRPPEDQEKKFADLRHRLTEETY
 RSKHHTLLKIHQYFGDLCSQLSRKDIMDFLKNENFDLVLDDMSDLCSSLIVEKLGKR
 FVSFLPFQFSYMDFGLPSAPLSYAPVYGSGLTDQMDFWGRVKNFLMFLDFSMKQREIL
 SQYDSTIQEHFVEGSQPVLSDLKAELWFVNDFALDFARPLFPNTVYVGGYWTNLF
 SQYPKTWRILSLSLETQVLSLWPWAL"

ORIGIN

Query Match 31.5%; Score 731.6; DB 3; Length 1353;
 Best Local Similarity 73.1%; Pred. No. 5.6e-196;
 Matches 981; Conservative 0; Mismatches 354; Indels 7; Gaps 3;

Qy	1	AGGGTCCCTAGCCGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGGCTCCGTAGA	60
Db	16	AGGGTCCCTAGTGGGGCACAGCTCTTAGGTGTGCAACCTGTGTCAGGGCTCCACATAT	75
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTCTAGTGGCTCCCTCTCCCTGGGTCT	120
Db	76	TCTACAGATGGCAGCACATCGGCCTGGCTCTCATGAGCTCCCTTGAGGTTAT	135
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	136	TCTCTGGAGGCTGCAAAAATCCTGACTATATCTACACTGAGTGCAAGCCATTATATAGT	195
Qy	181	GATGGACCGGGTTCTCAGATTCTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	196	GATAAGCCGTGTGCGCAAGTTCTCATGAAGGTGCCACAATGTGACCAAACCTCTTA	255
Qy	241	CAAAAGAGGTCTTTATGCCAGATTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	256	TGAAA---GTGCTAATATCCCAGATTAGAAAGGAAAACCATCATATCAAGTTATTAA	312
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTAAAAAGAGTTTGATTCTTCTGGA	360
Db	313	TTGGCGTCCACCTGAAGATCAGGAAAAGAAATTGCTGATCTTAGGCATCGACTACAGA	372
Qy	361	AGAAAACTTAGGTGGCAGAGGAAATTGAAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	373	AGAAAATAACTTATGGCAGGTCCAACATCACACCCCTCTAAAGATCCATCAATACTTGG	432
Qy	421	GTTGCAGTGCAGTCATTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAA	480
Db	433	GGACTTATGCAGTCAATTATTAAGCAGAAAGGACATCATGGACTCTTAAAGAATGAGAA	492
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTGACTACTGTCCTTCCTGATTGCTGAGAAGCT	540

Db	493	CTTGACCTAGTACTCTTGATTCAATGGATCTCTGTTCTTGCTAATTGTTGAAAGCT	552
Qy	541	TGGGAAGCCATTGTGGCCATTCTTCACTTCATTGGCTCTTGGAAATTGGCTACC	600
Db	553	TGGGAAACGATTGTGTCCTTCTTCCCTTCAATTAGCTATATGGACTTGGTTACC	612
Qy	601	AA---TCCCCTTGTCTTATGTTCCAGTATTCCGTCCTGCTGACTGATCACATGGACTT	657
Db	613	AAGGCCCGGCTTGTCCATTGCTCCAGTGTATGGTCTGGTCTAACTGACCAAATGGACTT	672
Qy	658	CTGGGGCCGAGTGAAGAATTCTGATGTTCTTAGTTCTGCAGGAGGCAACAGCACAT	717
Db	673	CTGGGGCCGAGTGAAGAACTTCTGATGTTCTTAGTTCTCCATGAAGCAAAGGAAAT	732
Qy	718	GCAGTCTACATTGACAACACCATCAAGGAACATTACAGAAGGCTCTAGGCCAGTTT	777
Db	733	CCTTCTCAGTATGACAGCACTATCCAGGAGCATTTGTGAAAGGCTCTAGCCAGTGT	792
Qy	778	GTCTCATCTTCTACTGAAAGCAGAGTTGTGGTCATTAACCTGACTTTGCCTTGATTT	837
Db	793	GTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTGTCAACTCTGACTTTGCTTGATTT	852
Qy	838	TGCTCGACCTCTGTTCCAACACTGTTATGTTGGAGGCTGATGGAAAAACCTATTAA	897
Db	853	TGCTCGTCCCCCTGTTCCAACACAGTCTATGTGGGAGG-TTACTGGACAAACCTGTC	911
Qy	898	ACCAAGTACCAAGACTTGGAGAACCTCATTGCCAAGTTGGGGACTCTGGTTTGTCC	957
Db	912	GCCAATACCCCAAGACTTGGAGAATTATCTCTCAGTTGGAGACTCAGGTTTGTCC	971
Qy	958	TGTGACCTGGGCTCCATGGTAACACCTGTCAGAATCCGAAATCTCAAGGAGATGAA	1017
Db	972	TGTGGCCTGGGCTCTATAGTGAGCATGATTCAAGGAAATTATAAGGAGATGAA	1031
Qy	1018	CAATGCCTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCACTGTTCTCATGGCC	1077
Db	1032	CAGTGCCTTGCTCACCTCCCTCAAGGGGTGCTATGGACATGTAAGACTCTCATGGCC	1091
Qy	1078	CAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCAGAGTGCACCT	1137
Db	1092	CAAAGATGTCAGTTGGCCCCAAATGTCAAATCATGGATTGGCTTCACAGACTGACCT	1151
Qy	1138	CCTGGCTCACCCAAAGCATCCGTCTGTTGTCACCCACGGCGGGCAGAATAGCATAATGGA	1197
Db	1152	TCTAGCTCACCTAGCATTGTCATGGAGGGATGAACAGTGTGATGGA	1211
Qy	1198	GGCCATCCAGCATGGTGTGCCCATGGTGGGATCCCTCTCTTGGAGACCAGCCTGAAAA	1257
Db	1212	GGCTGTCATCATGGAGTACCCATGGTGGGATTCCATTGACCAACCTGAAAA	1271
Qy	1258	CATGGTCCGAGTAGAAGCCAAAAGTTGGTGTTCATTCAAGTAAAGAAGCTCAAGGC	1317
Db	1272	CATGGTCCGAGTAGAAGCAAAGAACCTGGTGTTCATTCAAGCTACAGACGCTCAAGGC	1331
Qy	1318	AGAGACATTGGCTTAAAGATG	1339

Db 1332 AGAGTCATTCGCGCTCACCATG 1353

RESULT 9

BI102968

LOCUS BI102968 978 bp mRNA linear EST 26-JUN-2001
DEFINITION 602888578F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5043978
5', mRNA sequence.
ACCESSION BI102968
VERSION BI102968.1 GI:14553861
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 978)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11120 row: k column: 19
High quality sequence stop: 812.
FEATURES Location/Qualifiers
source 1. .978
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5043978"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Kid14"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"

ORIGIN

Query Match 22.5%; Score 522.4; DB 4; Length 978;
Best Local Similarity 77.7%; Pred. No. 1.6e-136;
Matches 682; Conservative 0; Mismatches 191; Indels 5; Gaps 4;

Qy 644 GATCACATGGACTTCTGGGGCCGAGTGAAGAATTTCTGATGTTCTTAGTTCTGCAGG 703
|| || ||||||| ||||||||| ||||||| ||||| ||||| ||| |

Db 1 GACCAAATGGACTTTGGGGCCGAGTGAAGAACATTCTGATGTTCTTCATTCACCAAG 60

Qy 704 AGGCAACAGCACATGCAGTCTACATTGACAACACCATCAAGGAACATTCACAGAAGGC 763
| || | | ||||| ||| || || ||| || || ||| ||| | |||||

Db 61 AAGCGAAGGGACATCTTCTCAATATGGCAATACTGTCCAGGAGCATTGCGGAAGGC 120

Qy	764	TCTAGGCCAGTTGTCTCATCTTACTGAAAGCAGAGTTGTGGTCATTAACCTGTAC	823
Db	121	TCTCAGGCCAGTGTGCTGACCTTACTGAAAGCTGAGCTGTGGTTGTCAACTCTGAC	180
Qy	824	TTTGCCTTGATTTGCTCGACCTCTGCTTCCAACACTGTTATGTTGGAGGCTTGATG	883
Db	181	TTTGCCTTGGATTTGCTCGTCCCTGTTCCAACACAGTCTATGTGGGAGGTTACTG	240
Qy	884	GAAAAACCTATTAAACCAGTACCACAAGACTGGAGAACATTGCAAGTTGGGAC	943
Db	241	GACAAACCTGTTAGCCAATACCCCAAGACTGGAGGATTTATCTCTCAGTTGGAGAC	300
Qy	944	TCTGGTTTGTCTTGACCTTGGCTCCATGGTAACACCTGTCAGAATCCGGAAATC	1003
Db	301	TCAGGTTTGTCTTGCCCTGGACTCTGTAGTGAGCATGATTCAAGGAAATT	360
Qy	1004	TTCAAGGAGATGAACAATGCCTTGCTCACCTACCCCAAGGGGTGATATGAAAGTGTCA	1063
Db	361	ATTAAGGAGATGAACAGTGCCTTGCTCACCTCCCTCAAGGGGTGCTATGGACATGTAAG	420
Qy	1064	TGTTCTCATTGGCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTT	1123
Db	421	AGTTCTCATTGGCCAAAGATGTCAAGTTGGCCCAAATGTCAAAATCATGGATTGGCTT	480
Qy	1124	CCTCAGAGTGACCTCCTGGCTACCCCAAGCATTGGCTGTTGTCACCCACGGCGGGCAG	1183
Db	481	CCACAGATTGACCTCTAGCTCACCTAGCATTGTCAGTTGTCACCCATGGGGGATG	540
Qy	1184	AATAGCATAATGGAGGCCATCCAGCATGGTGTGCCATGGGGGATCCCTCTTTGGA	1243
Db	541	AACAGTGTAAATGGAGGCTGTCCATCATGGAGTACCAATGGTAGGGATTCCATTGGGA	600
Qy	1244	GACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAGTTGGTGTTCATTCAAGTTA	1303
Db	601	GACCAACCTGAAAACATGGTCCGAGTAGAAGCAAAGAACCTGGTGTTCATTCAAGCTA	660
Qy	1304	AAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGAAAGACAAGAGA	1363
Db	661	CAGACACTCAAGGCAGAGTCATTGGCTCACCATGAAAGTCATAGAAGACCAGAGG	720
Qy	1364	TACAAGTCCCGGGCAGTGGCTGCCAGTGTCACTCTGCGCTCCACCCGCTCAGCCCCACA	1423
Db	721	TACAAGACTGCAGCA-TGGCCTCCAAGGTTATCAGGAACCTCCACC--AATGACCCCTGGC	777
Qy	1424	CAGCGGCTGGTGGCTGGATTGACCACGTC-CTCCAGACAGGGGGCGCAGCACCTCAA	1482
Db	778	CAGAGGCTTGTGGCTGGATTGATCACATCTTGCAGACAGGGGGTGCAGCCATCTCAA	837
Qy	1483	GCCCTATGTCTT-TCAGCAGCCCTGGCATGAGCACTAC	1519
Db	838	AGCATATGGCTTCCCAGCAGGCTTGGCATAACGAGTAC	875

RESULT 10

CN396939

LOCUS CN396939 510 bp mRNA linear EST 16-MAY-2004
 DEFINITION 17000599940872 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN396939
 VERSION CN396939.1 GI:47384534
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 510)
 AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
 Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
 Lebkowski,J and Stanton,L.W.
 TITLE Transcriptome characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
 COMMENT Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 Insert Length: 510 Std Error: 0.00.
 FEATURES Location/Qualifiers
 source 1. .510
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cell, retinoic acid and
 mitogen-treated hES cell line H7"
 /clone_lib="GRN_PRENEU"
 /note="oligo dT primed, full-length enriched cDNA library
 from hES cell line H7 (p29) maintained in feeder-free
 conditions. Embryoid bodies were generated in the presence
 of all-trans retinoic and mitogens."
 ORIGIN
 Query Match 21.8%; Score 506.4; DB 7; Length 510;
 Best Local Similarity 99.8%; Pred. No. 4.5e-132;
 Matches 507; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1109 ATTGTGGACTGGCTCCTCAGAGTGACCTCCTGGCTACCCAAGCATCCGTCTGTTGTC 1168
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 Db 3 ATTGTGGACTGGCTCCTCAGAGTGACCTCCTGGCTACCCAAGCATCCGTCTGTTGTC 62
 Qy 1169 ACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGG 1228
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 Db 63 ACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGG 122
 Qy 1229 ATCCCTCTCTTGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAGTTGGT 1288
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 Db 123 ATCCCTCTCTTGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAGTTGGT 182
 Qy 1289 GTTTCTATTCAAGTTAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATC 1348
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 183 GTTTCTATTCAAGTTAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATC 242
 Qy 1349 ATGGAAGACAAGAGATAACAAGTCCGCGGCAGTGGCTGCCAGTGTACATCCTGCGCTCCCAC 1408

Db	243	ATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTATCCTGCGCTCCCAC	302
Qy	1409	CCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCCCTCCAGACAGGGGGC	1468
Db	303	CCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCCCTCCAGACAGGGGGC	362
Qy	1469	GCGACGCACCTCAAGCCCTATGTCTTCAGCAGCCCTGGCATGAGCAGTACCTGTCGAC	1528
Db	363	GCGACGCACCTCAAGCCCTATGTCTTCAGCAGCCCTGGCATGAGCAGTACCTGTCGAC	422
Qy	1529	GTTTTGTGTTCTGCTGGGCTCACTCTGGGACTCTATGGCTTGTTGTGGAAAGCTGCTG	1588
Db	423	GTTTTGTGTTCTGCTGGGCTCACTCTGGGACTCTATGGCTTGTTGTGGAAAGCTGCTG	482
Qy	1589	GGCATGGCTGTCTGGTGGCTGCGTGGGG	1616
Db	483	GGCATGGCTGTCTGGTGGCTGCGTGGGG	510

RESULT 11

CR769328

LOCUS CR769328 717 bp mRNA linear EST 23-SEP-2004
 DEFINITION DKFZp46900528_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
 DKFZp46900528 5', mRNA sequence.
 ACCESSION CR769328
 VERSION CR769328.1 GI:52613343
 KEYWORDS EST.
 SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 REFERENCE 1 (bases 1 to 717)
 AUTHORS Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A.,
 Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
 Wiemann,S.
 TITLE Pongo pygmaeus mRNA (Ottenwaelder,B., Obermaier,B.,
 Deutschenbaur,S., et al.)
 JOURNAL Unpublished (2004)
 COMMENT Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);
 Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix
 (Martinsried/Germany) within the cDNA sequencing consortium of the
 German Genome Project. This clone (DKFZp46900528) is available at
 the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
 Berlin, Germany. Please contact RZPD for ordering:
<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp46900528>
 Further information about the clone and the sequencing project is
 available at <http://mips.gsf.de/projects/cdna/>.
 FEATURES Location/Qualifiers
 source 1. .717
 /organism="Pongo pygmaeus"
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/clone="DKFZp46900528"
/tissue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym: 'pkid1")
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"

ORIGIN

Query Match 21.1%; Score 490.6; DB 7; Length 717;
Best Local Similarity 83.1%; Pred. No. 1.6e-127;
Matches 593; Conservative 0; Mismatches 117; Indels 4; Gaps 3;

Qy 43 ATCCGGCGCTTCCGTAGAAGT GAGCATGGCTGGCAGCGAGT GCTTCTTAGT GGGCTT 102
Db 4 ATCCGGCGCTTGTGGAAGT GAGCATGGCTGGCAGCGGGTGCTGCTTAGT GGCCTT 63

Qy 103 CCTTCTCCCTGGGT CCTGCTCAGAGGCTGCCAAATCCTGACAATATCTACAGTAGG 162
Db 64 CCTTCTTTCTGGGT CCTGCTCAGAGGCTGCCAAATCCTGACAATATCTACACTGGG 123

Qy 163 TGGAAGCCATTATCTACTGATGGACCGGGTTCTCAGATTCTCAAGATCACGGTCATAA 222
Db 124 TGGAAGCCATTACCTACTGTTGGACCGGGTGTCTCAGATTCTCAAGAGCATGGTCATAA 183

Qy 223 TGTCAACCATGCTTAACCACAAAAGAGGT CCTTATGCCAGATTAAAAAGGAAGAAA 282
Db 184 TGTGACTATGCTTCATCAGAGTGGAAAGTTTAATCCAGATATTAAAGAGGAGGAAA 243

Qy 283 ATCATATCAAGTTATCAGTTGGCTTGCACCTGAAGATCATCAAAGAGAATTAAAAAGAG 342
Db 244 ATCATACCAAGTTATCAGGTGGTTTCACCTGAAGATTATCAAAAAGAATTAGAAGCA 303

Qy 343 TTTGATTTCTTCTGGAAGAAACTTGTGGCAGAGGAAATTGAAAACTTATTAAA 402
Db 304 TTTCGATAGTTACATAGAAACAGCATTGGATGGCAGAAAAGAATTGAAGTCTTGTAAA 363

Qy 403 TGTTCTAGAATACTTGGCGTTGCAGTCAGTCATTAAATAGAAAGGATATCATGGA 462
Db 364 GCTAATGGAAATATTGGGACTCAATGTAGTTATTGCTAACGAGAAAGGATATAATGGA 423

Qy 463 TTCCCTAAAGAATGAGAACCTTCGACATGGTGTAGTTGAAACTTTGACTACTGTCCTT 522
Db 424 TTCCCTAAAGAATGAAACTTTGATCTGGTATTGTTGAAGCATTGATTCTGTTCTT 483

Qy 523 CCTGATTGCTGAGAACGCTTGGGAAGCCATTGTGGCATTCTTCCACTTCATTGGCTC 582
Db 484 CCTGATTGCTGAGAACGCTTGTGAAACCATTGTGGCATTCTCCCACCACATTGGCTC 543

Qy 583 TTTGGAATTGGCTACCAATCCCCTGTCTTATGTTCCAGTATTCCGTTCTGCTGAC 642
Db 544 TTTGGATTTGGCTACCAAGCCCTTGTCTTATGTTCCAGTATTCCATTGCTGAC 603

Qy 643 TGATCACATGGACTTCT-GGGGCCGAGTGAAGAATTCTGATGTTCTTAGTTCTGCA 701
Db 604 TGATCACATGGACTTCTGGGGGCCGAGTGAAGAATTCTGATGNTCTTCTGAC 663

Qy 702 GGAGGC--AACAGCACATGCAGTCTACATT-GACAACACCATAAGGAACATT 752

Db 664 GGAGCCCAGGGACATGCAGTCTACATTGGACACNCCNTCAAGGAGCATT 717

RESULT 12

BI559553

LOCUS BI559553 761 bp mRNA linear EST 05-SEP-2001
DEFINITION 603252894F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5295502 5',
mRNA sequence.
ACCESSION BI559553
VERSION BI559553.1 GI:15446867
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 761)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11747 row: k column: 23
High quality sequence stop: 726.
FEATURES Location/Qualifiers
source 1. .761
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5295502"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XbaI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.2 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN

Query Match 21.1%; Score 488.6; DB 4; Length 761;
Best Local Similarity 80.7%; Pred. No. 6.1e-127;
Matches 608; Conservative 0; Mismatches 139; Indels 6; Gaps 3;

Qy 8 CTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGGCTTCCGTAGAAGTGAGC 67

Db	6	CTTAGCCCGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCTGCTTCTGTGGAAGTGAGC	65
Qy	68	ATGGCTGGGCAGCGAGTGCCTCTTCTAGTGGCTTCCCTGGGTCCCTGCTCTCA	127
Db	66	ATGGTGGCAGCGGGTGCCTAGTGGCTTCCCTCTTCTGGGTCCCTGCTCTCA	125
Qy	128	GAGGCTGCCAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGAC	187
Db	126	GAGGCTGCCAAATCCTGACAATATCTACACTGGGTGGAAGCCATTACCTACTGTTGGAC	185
Qy	188	CGGGTTCTCAGATTCTCAAGATCACGGTCATAATGTCACCATGCTAACCAACAAAAGA	247
Db	186	CGGGTGTCTCAGATTCTCAAGAGCATGGTCATAATGTGACTATGCTCATCAGAGTGG	245
Qy	248	GGTCCTTTATGCCAGATTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTT	307
Db	246	AAGTTTGGATCCAGATATTAAAGAGGAGGAAAAATCATACCAAGTTATCAGGTGGTT	305
Qy	308	GCACCTGAAGATCATCAAAGAGAATTAAAAAGAGTTGATTCTTCTGGAAGAAACT	367
Db	306	TCACCTGAAGATCATAAAAAAGAATTAAAGAGCATTGATAGCTACATAGAACAGCA	365
Qy	368	TTAGGTGGCAGAGGAAAATTGAAAACCTTATTAAATGTTCTAGAATACTTGGCGTTGCAG	427
Db	366	TTGGATGGCAGAAAAGAATCTGAAGGCCCTGTAAAGCTAATGGAAATTGGGACTCAA	425
Qy	428	TGCAGTCATTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAACTTCGAC	487
Db	426	TGTAGTTATTGCTAACGAGAAAGGATATAATGGATTCTTAAAGAATGAGAACTATGAT	485
Qy	488	ATGGTGATAGTTGAA-ACTTTGACTACTGTCCTTCTGATTGCTGAGAAGCTGGAA	546
Db	486	CTGGTATTGTTGAACGCATTGATTCTGTTCTTCTGATTGCTGAGAAGCTGTGAA	545
Qy	547	GCCATTGTGGCATTCTTCACTTCATTGGCTCTTGGAAATTGGCTACCAATCCC	606
Db	546	ACCATTGTGGCATTCTTCCCACCAATTGGCTCATGGATTGGGCTACCAAGCCC	605
Qy	607	CTTGTCTTATGTTCCAGTATTCCGTTCTGCTGACT-GATCACATGGACTTCTGGGCC	665
Db	606	CTTGTCTTATGTTCCAGTATTCCCTTCTGCTGACTGGATCACATGGACTTCTGGGCC	665
Qy	666	GAGTGAAGAATTCTGATGTTCTAGTTCTGCAGGAGG---CAACAGCACATGCAG	721
Db	666	GAGTGAAGAATTCTGATGTTCTAGTTCTCCAGGAGCCAAATGGGACATGCAG	725
Qy	722	TCTACATTGACAACACCATAAGGAACATTTC	754
Db	726	TCTACAATTGACAACACATAAGGAGCATTTC	758

RESULT 13

AW173071/c

LOCUS AW173071 694 bp mRNA linear EST 16-NOV-1999
DEFINITION xj82g11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2663780 3' similar to SW:CGT_RAT Q09426

2-HYDROXYACYLSPHINGOSINE 1-BETA-GALACTOSYLTRANSFERASE PRECURSOR ;,
mRNA sequence.

ACCESSION AW173071
VERSION AW173071.1 GI:6439019
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 694)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 412.
FEATURES Location/Qualifiers
source 1. .694
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2663780"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "

ORIGIN

Qy	448	AAAGGATATCATGGATTCTTAAAGAATGAGAACCTCGACATGGTATAGTTGAAACTT	507
Db	464	AAAGGATATAATGGATTCTTAAAGAATGAGAACATGATCTGGTATTGTTGAAGCATT	405
Qy	508	TGACTACTGCTCTTCTGATTGCTGAGAACGTTGGGAAGCCATTGTGCCATTCTTC	567
Db	404	TGATTCTGTTCTTCTGATTGCTGAGAACGTTGTGAAACCATTGTGCCATTCTCC	345
Qy	568	CACTTCATTGGCTCTTGGAAATTGGGCTACCAATCCCTGTCTATGTTCCAGTATT	627
Db	344	CACCACATTGGCTCTTGGATTGGCTACCAAGCCCTGTCTATGTTCCAGTATT	285
Qy	628	CCGTTCTTGCTGACTGATCACATGGACTCTGGGGCGAGTGAAGAATTCTGATGTT	687
Db	284	CCCTTCCTTGCTGACTGATCACATGGACTCTGGGGCGAGTGAAGAATTCTGATGTT	225
Qy	688	CTTTAGTTCTGCAGGAGGCAACACGACATGCAGTCTACATTGACAACACCATAAGGA	747
Db	224	CTTTAGTTCTCCAGGAGCCAATGGACATGCAGTCTACATTGACAACACCATAAGGA	165
Qy	748	ACATTCACAGAAGGCTCTAGGCCAGTTGTCTCATCTTCTACTGAAAGCAGAGTTGTG	807
Db	164	GCATTCCCAGAAGGCTCTAGGCCAGTTGTCTCATCTTCTACTGAAAGCAGAGTTGTG	105
Qy	808	GTTCATTAACCTTGACTTGCCTTGATTGCTCGACCTCTGCTTCCAACACTGTTA	867
Db	104	GTGGTTAACTCTGATTGCTTGATTGCTTGCCTTGATTGCCCCGCTGCTTCCAACACTGTTA	45
Qy	868	TGTTGGAGGCTTGATGGAAAAACCTATTAAACCAAGTACCAACAA	910
Db	44	TATTGGAGGCTTGATGGAAAAACCTATTAAACCAAGTACCAACAA	2

RESULT 14

CB435346/c

LOCUS CB435346 659 bp mRNA linear EST 25-MAR-2003
 DEFINITION 615435 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.
 ACCESSION CB435346
 VERSION CB435346.1 GI:29216283
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 REFERENCE 1 (bases 1 to 659)
 AUTHORS Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G.,
 Wray, J.E. and Keele, J.W.
 TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
 JOURNAL Unpublished (2003)
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329.

Plate: FOY8035 row: J column: 24

Seq primer: TAGAAGGCACAGTCGAGG.

FEATURES Location/Qualifiers
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/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."

ORIGIN

RESULT 15

AK052644

LOCUS AK052644 **1723 bp mRNA linear HTC 03-APR-2004**
DEFINITION Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630011D02 product:hypothetical UDP-glucuronosyl and UDP-glucosyl transferase containing protein, full insert sequence.
ACCESSION AK052644
VERSION AK052644.1 GI:26095303
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 1723)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:<http://genome.gsc.riken.jp/>, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:<http://genome.gsc.riken.jp/>
URL:<http://fantom.gsc.riken.jp/>.
FEATURES
source Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:D630011D02"
/db_xref="taxon:10090"
/clone="D630011D02"
/tissue_type="kidney"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
misc_feature
1. .1723
/note="hypothetical UDP-glucuronosyl and UDP-glucosyl transferase containing protein (InterPro|IPR002213, evidence: InterPro)"

ORIGIN

Query Match 19.5%; Score 452.6; DB 3; Length 1723;
 Best Local Similarity 69.1%; Pred. No. 1.5e-116;
 Matches 649; Conservative 0; Mismatches 284; Indels 6; Gaps 2;

Qy 1 AGGGTCCCTTAGCCGGCGCAGGGCGCGAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Db	41	AGGGTCCCTTAGTGGGCACAGCTCTTAGGTGTGCAACCTGTGTCAGGGCTCCACATAT	100
Qy	61	AGT GAGC ATGGCTGGGCAGCGAGTGCTTCTTAGTGGCTTCCCTCTCCCTGGGTCC	120
Db	101	TCTACAGATGGCAGCACATCGGCAGTGGCTCATGAGCTCCTTCCCTGAGGTAT	160
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	161	TCTCTTGGAGGCTGCAAAAATCCTGACTATATCTACACTGAGTGCAAGCCATTATATAGT	220
Qy	181	GATGGACCGGGTTCTCAGATTCTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	221	GATAAGCCGTGTGTCGCAAGTTCTCATGAAGGTGGCCACAATGTGACCAAACCTTTA	280
Qy	241	CAAAAGAGGTCTTTATGCCAGATTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	281	TGAAA---GTGCTAATATCCCAGATTTAGAAAGGAAAACCATCATATCAAGTTATTAA	337
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTAAAAAGAGTTTGATTCTTCTGGA	360
Db	338	TTGGCGTCCACCTGAAGATCAGGAAAAGAAATTGCTGATCTTAGGCATCGACTTACAGA	397
Qy	361	AGAAAACTTAGGTGGCAGAGGAAATTGAAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	398	AGAAAATAACTTATGGCAGGTCCAAACATCACACCCCTCTAAAGATCCATCAATACTTGG	457
Qy	421	GTTGCAGTGCAGTCATTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAA	480
Db	458	GGACTTATGCAGTCATTATTAAAGCAGAAAGGACATCATGGACTCTTAAAGATGAGAA	517
Qy	481	CTTCGACATGGTGTAGTTGAAACCTTGTACTGTCTTCTGATTGCTGAGAAGCT	540
Db	518	CTTGACCTAGTACTTCTGATTCAATGGATCTCTGTCTTGCTAATTGTTGAAAAGCT	577
Qy	541	TGGGAAGCCATTGTGGCATTCTTCACTTCATTGGCTCTTGGATTGGCTACC	600
Db	578	TGGGAAACGATTGTGTCCTTCTCCCTTCAATTAGCTATATGGACTTGGTTTAC	637
Qy	601	AA---TCCCCTGTCTTATGTTCCAGTATTCCGTTCTGCTGACTGATCACATGGACTT	657
Db	638	AAGCGCCCCCTGTCCATGCTCCAGTGTATGGTTCTGGCTAACTGACCAATGGACTT	697
Qy	658	CTGGGGCCGAGTGAAGAATTCTGTATGTTCTTAGTTCTGCTGAGGAGGCAACAGCACAT	717
Db	698	CTGGGGCCGAGTGAAGAACTTCTGATGTTCTGATTCTCCATGAAGCAAAGGAAAT	757
Qy	718	GCAGTCTACATTGACAACACCATCAAGGAACATTCACAGAAGGCTCTAGGCCAGTTT	777
Db	758	CCTTTCTCAGTATGACAGCACTATCCAGGAGCATTGTGGAAAGGCTCTAGCCAGTGT	817
Qy	778	GTCTCATCTTCTACTGAAAGCAGAGTTGTGGTCATTAACCTGACTTGCCTTGATTT	837
Db	818	GTCTGACCTCTACTGAAAGCTGAGCTGTGGTTGTCAACTCTGACTTGCCTTGATTT	877
Qy	838	TGCTCGACCTCTGCTTCCAAACACTGTTATGTTGGAGGCTTGATGGAAAAACCTATTAA	897
Db	878	TGCTCGTCCCCTGTTCCAAACACAGTCTATGTGGAGGTTACTGGACAAACCTGTTCA	937

Qy 898 ACCAGTACCACAAGACTTGGAGAACATTGCCAAGTT 936
||| |||| |||| ||| ||| || | || |||
Db 938 GCCAATACCCCAAGTAAGTGACAAATTAGCTCTCACTTT 976

Search completed: February 15, 2005, 09:44:23
Job time : 6858 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2005, 06:24:06 ; Search time 4625 Seconds
(without alignments)
2959.798 Million cell updates/sec

Title: US-10-017-867A-281
Perfect score: 2320
Sequence: 1 agggtccttagccgggcgc.....tctctcccaacctcactaa 2320

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5378673 seqs, 2950229984 residues

Total number of hits satisfying chosen parameters: 10757346

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published_Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description	
	No.	Score	Match	Length	DB ID		
	37	2320	100.0	2320	16	US-10-013-909A-281	Sequence 281, App
	66	2102.8	90.6	2944	17	US-10-468-125-13	Sequence 13, Appl
	67	2063.4	88.9	2074	9	US-09-822-830A-262	Sequence 262, App
	68	1578.8	68.1	2263	17	US-10-381-898-31	Sequence 31, Appl
	69	1281.6	55.2	2082	9	US-09-895-728-1	Sequence 1, Appli
	70	1281.6	55.2	2823	17	US-10-094-749-1288	Sequence 1288, Ap
	71	1280	55.2	2086	17	US-10-258-080-12	Sequence 12, Appl
	72	1270.4	54.8	1851	9	US-09-740-029-1	Sequence 1, Appli
	73	1212	52.2	1572	9	US-09-895-728-3	Sequence 3, Appli
	74	1147.8	49.5	2426	17	US-10-120-988-26	Sequence 26, Appl
c	75	708.2	30.5	1898	17	US-10-276-774-1313	Sequence 1313, Ap
	76	593.4	25.6	1842	17	US-10-104-047-811	Sequence 811, App
c	77	441	19.0	923	17	US-10-295-027-677	Sequence 677, App
	78	433.6	18.7	42999	9	US-09-740-029-3	Sequence 3, Appli
	79	319.4	13.8	981	10	US-09-764-891-1668	Sequence 1668, Ap
	80	239.2	10.3	5973	10	US-09-764-891-8352	Sequence 8352, Ap
c	81	238.8	10.3	507	9	US-09-864-761-13591	Sequence 13591, A
	82	238.8	10.3	2751	10	US-09-764-891-8351	Sequence 8351, Ap
	83	238.8	10.3	5974	10	US-09-764-891-8353	Sequence 8353, Ap
c	84	220	9.5	277	9	US-09-864-761-30130	Sequence 30130, A
	85	164.2	7.1	708	13	US-10-027-632-98682	Sequence 98682, A
	86	164.2	7.1	708	17	US-10-027-632-98682	Sequence 98682, A
	87	162.6	7.0	49753	13	US-10-087-192-1855	Sequence 1855, Ap
	88	159.6	6.9	625	13	US-10-027-632-95784	Sequence 95784, A
	89	159.6	6.9	625	13	US-10-027-632-95785	Sequence 95785, A
	90	159.6	6.9	625	13	US-10-027-632-95786	Sequence 95786, A
	91	159.6	6.9	625	17	US-10-027-632-95784	Sequence 95784, A
	92	159.6	6.9	625	17	US-10-027-632-95785	Sequence 95785, A
	93	159.6	6.9	625	17	US-10-027-632-95786	Sequence 95786, A
	94	145.2	6.3	1961	9	US-09-917-800A-1403	Sequence 1403, Ap
	95	144.2	6.2	1584	9	US-09-962-678-3	Sequence 3, Appli
	96	144.2	6.2	1584	17	US-10-184-648-40	Sequence 40, Appl
	97	144.2	6.2	3006	9	US-09-962-678-1	Sequence 1, Appli
	98	144.2	6.2	3006	17	US-10-184-648-38	Sequence 38, Appl
	99	143.2	6.2	1636	9	US-09-981-353-165	Sequence 165, App
	100	143.2	6.2	1636	17	US-10-258-080-11	Sequence 11, Appl
	101	143.2	6.2	2966	9	US-09-981-353-33	Sequence 33, Appl
	564	143.2	6.2	2974	16	US-10-174-587-521	Sequence 521, App
	621	143.2	6.2	2974	18	US-10-643-795A-3	Sequence 3, Appli
	622	141.8	6.1	336	11	US-09-864-408A-941	Sequence 941, App
	623	141.8	6.1	1947	17	US-10-152-319A-2121	Sequence 2121, Ap
	624	141.6	6.1	1705	17	US-10-114-270-51	Sequence 51, Appl
	625	141.2	6.1	1620	14	US-10-158-646-45	Sequence 45, Appl
	626	141	6.1	3050	17	US-10-114-270-49	Sequence 49, Appl
	627	140	6.0	1593	17	US-10-152-319A-1908	Sequence 1908, Ap
	628	140	6.0	2634	17	US-10-388-934-169	Sequence 169, App
	629	139.8	6.0	1639	17	US-10-468-125-18	Sequence 18, Appl
	630	139.2	6.0	1714	9	US-09-981-353-193	Sequence 193, App
	631	139.2	6.0	1855	9	US-09-880-107-2120	Sequence 2120, Ap
	632	139.2	6.0	1855	11	US-09-968-007A-368	Sequence 368, App
	633	139.2	6.0	1855	11	US-09-968-007A-735	Sequence 735, App
	634	139.2	6.0	1855	18	US-10-783-528-57	Sequence 57, Appl
	635	139.2	6.0	1991	14	US-10-057-834A-1	Sequence 1, Appli

636	136.4	5.9	1844	14	US-10-175-523-59	Sequence 59, Appl
637	136.4	5.9	2448	9	US-09-967-768A-187	Sequence 187, App
638	136	5.9	1854	14	US-10-205-522-39	Sequence 39, Appl
639	133.8	5.8	1894	17	US-10-172-118-904	Sequence 904, App
640	133.8	5.8	1894	17	US-10-342-887-904	Sequence 904, App
641	133.4	5.8	1756	15	US-10-235-994-27	Sequence 27, Appl
642	133.2	5.7	1829	16	US-10-252-157-24	Sequence 24, Appl
643	133	5.7	1662	17	US-10-307-817-117	Sequence 117, App
644	132	5.7	1614	17	US-10-381-898-24	Sequence 24, Appl
645	131.6	5.7	2092	14	US-10-205-522-7	Sequence 7, Appl
646	130	5.6	2123	9	US-09-880-107-3286	Sequence 3286, Ap
647	129	5.6	2799	9	US-09-880-107-3756	Sequence 3756, Ap
648	128.4	5.5	1976	14	US-10-205-522-112	Sequence 112, App
649	128.4	5.5	2090	9	US-09-880-107-3292	Sequence 3292, Ap
650	127.6	5.5	1413	13	US-10-060-311-1	Sequence 1, Appl
651	127.6	5.5	1413	18	US-10-778-300-1	Sequence 1, Appl
652	127.2	5.5	2150	9	US-09-981-353-45	Sequence 45, Appl
653	127.2	5.5	2150	16	US-10-252-157-25	Sequence 25, Appl
654	125.2	5.4	2093	9	US-09-880-107-3842	Sequence 3842, Ap
655	124.2	5.4	2844	14	US-10-198-846-13134	Sequence 13134, A
656	124	5.3	1889	9	US-09-981-353-83	Sequence 83, Appl
657	121.2	5.2	1712	9	US-09-981-353-189	Sequence 189, App
658	121.2	5.2	1712	14	US-10-158-646-42	Sequence 42, Appl
659	120.6	5.2	1224	17	US-10-381-898-32	Sequence 32, Appl
660	119.6	5.2	2349	9	US-09-981-353-151	Sequence 151, App
661	119.6	5.2	2349	13	US-10-044-090-845	Sequence 845, App
662	115.8	5.0	2422	9	US-09-880-107-2106	Sequence 2106, Ap
663	115.8	5.0	2422	11	US-09-968-007A-750	Sequence 750, App
664	112.8	4.9	2368	17	US-10-240-425-1321	Sequence 1321, Ap
665	112.8	4.9	2380	13	US-10-044-090-816	Sequence 816, App
666	112.8	4.9	2385	9	US-09-981-353-153	Sequence 153, App
667	111.4	4.8	2320	9	US-09-835-082-1	Sequence 1, Appl
668	111.4	4.8	2320	9	US-09-835-082-3	Sequence 3, Appl
669	111.4	4.8	2320	17	US-10-333-108-6	Sequence 6, Appl
670	111.4	4.8	2320	18	US-10-422-522-35	Sequence 35, Appl
671	111	4.8	1593	18	US-10-250-508-18	Sequence 18, Appl
672	111	4.8	1593	18	US-10-250-508-19	Sequence 19, Appl
673	111	4.8	1593	18	US-10-250-508-20	Sequence 20, Appl
674	111	4.8	1593	18	US-10-250-508-21	Sequence 21, Appl
675	110	4.7	811	14	US-10-198-846-10821	Sequence 10821, A
676	97	4.2	1593	17	US-10-152-319A-2064	Sequence 2064, Ap
677	95.6	4.1	735	9	US-09-305-856B-17	Sequence 17, Appl
678	95.6	4.1	735	16	US-10-247-159-17	Sequence 17, Appl
679	93.2	4.0	54493	13	US-10-087-192-1858	Sequence 1858, Ap
680	86.2	3.7	419	9	US-09-960-352-9640	Sequence 9640, Ap
681	86.2	3.7	874	17	US-10-332-859-134	Sequence 134, App
682	86.2	3.7	1318	17	US-10-332-859-296	Sequence 296, App
683	76.8	3.3	426	9	US-09-960-352-13860	Sequence 13860, A
684	75.8	3.3	418	9	US-09-960-352-10064	Sequence 10064, A
685	74.6	3.2	603	9	US-09-917-800A-1434	Sequence 1434, Ap
686	74	3.2	582	9	US-09-867-701-1453	Sequence 1453, Ap
c 687	73.8	3.2	918	13	US-10-027-632-146775	Sequence 146775,
c 688	73.8	3.2	918	17	US-10-027-632-146775	Sequence 146775,
689	72	3.1	450	14	US-10-198-846-1381	Sequence 1381, Ap
690	70.8	3.1	601	9	US-09-917-800A-1433	Sequence 1433, Ap
691	69.2	3.0	350	9	US-09-960-352-2069	Sequence 2069, Ap
692	69.2	3.0	381	9	US-09-960-352-2070	Sequence 2070, Ap

693	66.8	2.9	416	9	US-09-960-352-12236	Sequence 12236, A
694	63.8	2.8	500	9	US-09-864-761-8163	Sequence 8163, Ap
695	63.8	2.8	689	14	US-10-205-522-5	Sequence 5, Appli
696	63.6	2.7	370	9	US-09-960-352-3236	Sequence 3236, Ap
697	63.4	2.7	378	9	US-09-960-352-1300	Sequence 1300, Ap
698	63.4	2.7	396	14	US-10-066-543-2912	Sequence 2912, Ap
699	63.4	2.7	569	13	US-10-027-632-187724	Sequence 187724,
700	63.4	2.7	569	17	US-10-027-632-187724	Sequence 187724,
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702	62.4	2.7	391	9	US-09-854-133-21	Sequence 21, Appl
703	62.4	2.7	391	15	US-10-144-649A-21	Sequence 21, Appl
704	62.4	2.7	417	9	US-09-960-352-11024	Sequence 11024, A
705	62.2	2.7	1591	14	US-10-205-522-44	Sequence 44, Appl
706	60.8	2.6	1751	18	US-10-437-963-38200	Sequence 38200, A
707	60.2	2.6	196	9	US-09-960-352-3013	Sequence 3013, Ap
708	60	2.6	220	9	US-09-864-761-24905	Sequence 24905, A
709	59.4	2.6	1606	17	US-10-042-865-27	Sequence 27, Appl
710	59.4	2.6	1606	17	US-10-072-012-151	Sequence 151, App
c 711	59	2.5	589	9	US-09-864-761-14859	Sequence 14859, A
c 712	58.6	2.5	753	18	US-10-425-115-95645	Sequence 95645, A
713	58.6	2.5	1555	18	US-10-437-963-83376	Sequence 83376, A
c 714	58.6	2.5	2071	18	US-10-739-930-2568	Sequence 2568, Ap
715	58.2	2.5	432	14	US-10-066-543-3166	Sequence 3166, Ap
716	57.4	2.5	1515	18	US-10-437-963-97778	Sequence 97778, A
717	57.2	2.5	646	18	US-10-767-701-1823	Sequence 1823, Ap
718	56.8	2.4	987	17	US-10-425-114-31066	Sequence 31066, A
719	56.8	2.4	1391	17	US-10-425-114-20377	Sequence 20377, A
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721	56.8	2.4	1761	18	US-10-739-930-2527	Sequence 2527, Ap
722	56.2	2.4	983	17	US-10-294-934-386	Sequence 386, App
723	55.4	2.4	1637	18	US-10-425-115-174192	Sequence 174192,
c 724	55.2	2.4	203	9	US-09-864-761-31386	Sequence 31386, A
725	55.2	2.4	2541	18	US-10-425-115-174195	Sequence 174195,
726	55	2.4	1602	14	US-10-205-522-117	Sequence 117, App
727	54.2	2.3	1380	16	US-10-167-547C-21	Sequence 21, Appl
728	53.8	2.3	531	15	US-10-259-165-700	Sequence 700, App
729	53.8	2.3	849	18	US-10-425-115-32911	Sequence 32911, A
730	53.8	2.3	1380	16	US-10-167-547C-23	Sequence 23, Appl
731	53.8	2.3	1904	17	US-10-424-599-106506	Sequence 106506,
732	53.4	2.3	577	16	US-10-029-386-13232	Sequence 13232, A
733	53.4	2.3	629	18	US-10-767-701-24016	Sequence 24016, A
734	53.4	2.3	784	17	US-10-333-108-8	Sequence 8, Appli
735	53.4	2.3	1701	17	US-10-425-114-28222	Sequence 28222, A
736	53.4	2.3	1705	18	US-10-425-115-137865	Sequence 137865,
737	53.4	2.3	17483	18	US-10-751-606-1	Sequence 1, Appli
738	53.2	2.3	393	9	US-09-960-352-8259	Sequence 8259, Ap
739	53.2	2.3	549	18	US-10-437-963-18130	Sequence 18130, A
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741	52.8	2.3	383	9	US-09-960-352-1313	Sequence 1313, Ap
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743	52	2.2	707	18	US-10-357-930-24702	Sequence 24702, A
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745	51.8	2.2	963	17	US-10-425-114-19881	Sequence 19881, A
746	51.8	2.2	1688	17	US-10-425-114-23090	Sequence 23090, A
747	51.8	2.2	1952	18	US-10-425-115-38737	Sequence 38737, A
748	51.6	2.2	405	18	US-10-425-115-11581	Sequence 11581, A
749	51.6	2.2	781	18	US-10-425-115-154997	Sequence 154997,

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754	51.2	2.2	1536	17	US-10-425-114-13903	Sequence 13903, A
755	51.2	2.2	1585	18	US-10-425-115-83913	Sequence 83913, A
756	51	2.2	1428	18	US-10-437-963-48509	Sequence 48509, A
757	51	2.2	1741	17	US-10-425-114-17536	Sequence 17536, A
c 758	51	2.2	1924	18	US-10-437-963-36431	Sequence 36431, A
759	51	2.2	2041	18	US-10-425-115-41669	Sequence 41669, A
c 760	50.8	2.2	1090	18	US-10-767-701-9917	Sequence 9917, Ap
c 761	50.8	2.2	1708	18	US-10-425-115-6686	Sequence 6686, Ap
762	50.6	2.2	1409	18	US-10-437-963-26987	Sequence 26987, A
763	50.4	2.2	493	18	US-10-767-701-29807	Sequence 29807, A
764	50.4	2.2	647	18	US-10-767-701-7103	Sequence 7103, Ap
765	50.4	2.2	1064	18	US-10-767-701-6787	Sequence 6787, Ap
766	50.4	2.2	1536	17	US-10-359-369-21	Sequence 21, Appl
767	50.4	2.2	1575	17	US-10-359-369-26	Sequence 26, Appl
c 768	50.4	2.2	1582	18	US-10-437-963-54318	Sequence 54318, A
769	50.4	2.2	1601	13	US-10-078-929-71	Sequence 71, Appl
770	50.2	2.2	627	15	US-10-259-165-135	Sequence 135, App
771	50.2	2.2	659	18	US-10-425-115-49556	Sequence 49556, A
772	50.2	2.2	1389	17	US-10-424-599-64785	Sequence 64785, A
773	50.2	2.2	1511	18	US-10-437-963-99212	Sequence 99212, A
c 774	50.2	2.2	1649	18	US-10-739-930-2332	Sequence 2332, Ap
775	50	2.2	947	18	US-10-739-930-3855	Sequence 3855, Ap
776	50	2.2	1052	17	US-10-425-114-24020	Sequence 24020, A
777	50	2.2	1358	18	US-10-425-115-146230	Sequence 146230,
778	49.8	2.1	743	18	US-10-425-115-125571	Sequence 125571,
779	49.8	2.1	1711	18	US-10-739-930-2421	Sequence 2421, Ap
780	49.6	2.1	398	13	US-10-078-929-67	Sequence 67, Appl
781	49.6	2.1	563	18	US-10-357-930-37283	Sequence 37283, A
782	49.6	2.1	932	13	US-10-078-929-65	Sequence 65, Appl
783	49.6	2.1	1603	17	US-10-425-114-34547	Sequence 34547, A
784	49.6	2.1	1627	17	US-10-425-114-20731	Sequence 20731, A
785	49.6	2.1	1840	18	US-10-425-115-126489	Sequence 126489,
c 786	49.2	2.1	600	18	US-10-425-115-81788	Sequence 81788, A
787	49.2	2.1	656	9	US-09-768-020-77	Sequence 77, Appl
788	49.2	2.1	657	14	US-10-255-536-104	Sequence 104, App
789	49.2	2.1	891	17	US-10-425-114-30590	Sequence 30590, A
790	49.2	2.1	1619	17	US-10-425-114-21697	Sequence 21697, A
791	49.2	2.1	1784	18	US-10-425-115-136164	Sequence 136164,
792	49.2	2.1	1807	17	US-10-425-114-28103	Sequence 28103, A
793	49.2	2.1	1943	18	US-10-425-115-122168	Sequence 122168,
794	49	2.1	501	18	US-10-357-930-7320	Sequence 7320, Ap
795	49	2.1	1052	15	US-10-259-165-668	Sequence 668, App
c 796	49	2.1	1058	18	US-10-767-701-6477	Sequence 6477, Ap
797	49	2.1	1491	18	US-10-437-963-52288	Sequence 52288, A
c 798	48.8	2.1	558	11	US-09-969-034-4441	Sequence 4441, Ap
799	48.8	2.1	1448	17	US-10-425-114-23975	Sequence 23975, A
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c 801	48.6	2.1	875	18	US-10-437-963-54314	Sequence 54314, A
802	48.6	2.1	1001	17	US-10-294-934-404	Sequence 404, App
803	48.6	2.1	1647	18	US-10-739-930-2506	Sequence 2506, Ap
804	48.6	2.1	2142	18	US-10-437-963-26615	Sequence 26615, A
805	48.4	2.1	1437	9	US-09-938-842A-200	Sequence 200, App
806	48.4	2.1	1437	11	US-09-938-842A-200	Sequence 200, App

807	48.4	2.1	1638	17	US-10-425-114-1736	Sequence 1736, Ap
808	48.4	2.1	1785	18	US-10-739-930-2178	Sequence 2178, Ap
c 809	48.4	2.1	1796	18	US-10-437-963-15077	Sequence 15077, A
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c 811	48.2	2.1	551	15	US-10-259-165-483	Sequence 483, App
c 812	48.2	2.1	551	17	US-10-260-238-4854	Sequence 4854, Ap
813	48.2	2.1	916	17	US-10-425-114-14455	Sequence 14455, A
814	48.2	2.1	1827	17	US-10-425-114-21585	Sequence 21585, A
815	48.2	2.1	2112	18	US-10-425-115-57104	Sequence 57104, A
816	48	2.1	666	18	US-10-767-701-3341	Sequence 3341, Ap
817	48	2.1	1494	18	US-10-437-963-61715	Sequence 61715, A
818	48	2.1	1560	18	US-10-437-963-55774	Sequence 55774, A
819	48	2.1	1630	17	US-10-425-114-35120	Sequence 35120, A
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822	47.8	2.1	1461	18	US-10-437-963-80973	Sequence 80973, A
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c 826	47.6	2.1	706	17	US-10-424-599-139514	Sequence 139514,
827	47.6	2.1	1485	17	US-10-425-114-23053	Sequence 23053, A
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829	47.6	2.1	1805	18	US-10-739-930-4281	Sequence 4281, Ap
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833	47.2	2.0	1882	17	US-10-425-114-15891	Sequence 15891, A
834	47.2	2.0	1902	18	US-10-425-115-130862	Sequence 130862,
c 835	47	2.0	523	18	US-10-425-115-84886	Sequence 84886, A
836	47	2.0	1455	18	US-10-437-963-8361	Sequence 8361, Ap
837	47	2.0	1746	17	US-10-425-114-32779	Sequence 32779, A
838	46.8	2.0	429	18	US-10-767-701-2000	Sequence 2000, Ap
839	46.8	2.0	629	18	US-10-767-701-7057	Sequence 7057, Ap
840	46.6	2.0	334	9	US-09-981-353-149	Sequence 149, App
841	46.6	2.0	334	14	US-10-158-646-43	Sequence 43, Appl
c 842	46.6	2.0	634	15	US-10-259-165-476	Sequence 476, App
843	46.6	2.0	1416	18	US-10-425-115-90291	Sequence 90291, A
844	46.6	2.0	2050	18	US-10-767-701-13466	Sequence 13466, A
845	46.4	2.0	315	9	US-09-960-352-5852	Sequence 5852, Ap
846	46.4	2.0	1440	9	US-09-938-842A-80	Sequence 80, Appl
847	46.4	2.0	1440	11	US-09-938-842A-80	Sequence 80, Appl
848	46.4	2.0	1440	17	US-10-359-369-11	Sequence 11, Appl
849	46.4	2.0	1440	17	US-10-203-319A-10	Sequence 10, Appl
c 850	46.4	2.0	1440	17	US-10-203-319A-12	Sequence 12, Appl
851	46.4	2.0	1865	18	US-10-739-930-1152	Sequence 1152, Ap
852	46.2	2.0	1410	18	US-10-437-963-97054	Sequence 97054, A
853	46.2	2.0	1430	17	US-10-425-114-27279	Sequence 27279, A
854	46.2	2.0	1464	18	US-10-425-115-100628	Sequence 100628,
855	46.2	2.0	1694	18	US-10-437-963-42666	Sequence 42666, A
856	46.2	2.0	1762	17	US-10-425-114-27635	Sequence 27635, A
857	46.2	2.0	1999	18	US-10-437-963-85175	Sequence 85175, A
858	46	2.0	1557	18	US-10-437-963-18533	Sequence 18533, A
859	46	2.0	1973	18	US-10-437-963-97633	Sequence 97633, A
860	45.8	2.0	592	18	US-10-425-115-117281	Sequence 117281,
861	45.8	2.0	1188	18	US-10-437-963-101308	Sequence 101308,
862	45.8	2.0	1353	18	US-10-437-963-47687	Sequence 47687, A
863	45.8	2.0	1395	18	US-10-437-963-101310	Sequence 101310,

864	45.8	2.0	1473	18	US-10-437-963-47689	Sequence 47689, A
865	45.8	2.0	13511	15	US-10-311-455-254	Sequence 254, App
866	45.8	2.0	18585	15	US-10-240-485-162	Sequence 162, App
867	45.6	2.0	1770	17	US-10-425-114-15851	Sequence 15851, A
868	45.6	2.0	1780	18	US-10-425-115-181935	Sequence 181935,
869	45.6	2.0	2319	18	US-10-437-963-50152	Sequence 50152, A
870	45.4	2.0	614	18	US-10-767-701-875	Sequence 875, App
871	45.4	2.0	661	18	US-10-767-701-4653	Sequence 4653, Ap
872	45.4	2.0	1674	17	US-10-425-114-15925	Sequence 15925, A
873	45.4	2.0	1699	18	US-10-437-963-52771	Sequence 52771, A
874	45.4	2.0	1722	18	US-10-425-115-168238	Sequence 168238,
875	45.2	1.9	242	9	US-09-923-876-847	Sequence 847, App
876	45.2	1.9	242	10	US-09-923-876-847	Sequence 847, App
c 877	45.2	1.9	507	18	US-10-425-115-180382	Sequence 180382,
878	45.2	1.9	1624	17	US-10-425-114-15834	Sequence 15834, A
879	45.2	1.9	1634	18	US-10-425-115-180642	Sequence 180642,
880	45.2	1.9	1728	18	US-10-425-115-56280	Sequence 56280, A
881	45.2	1.9	1736	13	US-10-078-929-79	Sequence 79, Appl
882	45.2	1.9	1796	18	US-10-437-963-7426	Sequence 7426, Ap
883	45.2	1.9	5335	18	US-10-437-963-18859	Sequence 18859, A
920	45	1.9	45	16	US-10-013-909A-285	Sequence 285, App
949	45	1.9	503	18	US-10-425-115-89379	Sequence 89379, A
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951	45	1.9	1536	9	US-09-773-882-10	Sequence 10, Appl
952	45	1.9	1560	17	US-10-359-369-33	Sequence 33, Appl
953	45	1.9	1732	9	US-09-773-882-1	Sequence 1, Appli
954	44.8	1.9	1362	9	US-09-938-842A-2417	Sequence 2417, Ap
955	44.8	1.9	1362	11	US-09-938-842A-2417	Sequence 2417, Ap
956	44.8	1.9	1473	18	US-10-437-963-70764	Sequence 70764, A
957	44.8	1.9	1867	18	US-10-437-963-41728	Sequence 41728, A
958	44.8	1.9	2323	18	US-10-437-963-88877	Sequence 88877, A
c 959	44.6	1.9	661	18	US-10-425-115-119313	Sequence 119313,
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961	44.6	1.9	1437	17	US-10-359-369-17	Sequence 17, Appl
c 962	44.6	1.9	1803	18	US-10-425-115-109154	Sequence 109154,
963	44.6	1.9	2532	18	US-10-437-963-80263	Sequence 80263, A
c 964	44.4	1.9	1607	18	US-10-425-115-58267	Sequence 58267, A
965	44.4	1.9	2166	17	US-10-425-114-18441	Sequence 18441, A
966	44.2	1.9	314	18	US-10-425-115-115658	Sequence 115658,
c 967	44.2	1.9	576	18	US-10-425-115-122874	Sequence 122874,
968	44.2	1.9	1449	18	US-10-437-963-33526	Sequence 33526, A
969	44.2	1.9	3750	18	US-10-437-963-53143	Sequence 53143, A
970	44	1.9	481	17	US-10-425-114-3555	Sequence 3555, Ap
971	44	1.9	1593	18	US-10-437-963-40777	Sequence 40777, A
972	44	1.9	1696	17	US-10-425-114-28610	Sequence 28610, A
973	44	1.9	1811	18	US-10-425-115-95638	Sequence 95638, A
974	43.8	1.9	1152	15	US-10-259-165-201	Sequence 201, App
975	43.8	1.9	1494	18	US-10-437-963-95025	Sequence 95025, A
976	43.8	1.9	1594	17	US-10-424-599-8655	Sequence 8655, Ap
977	43.8	1.9	1660	17	US-10-425-114-24406	Sequence 24406, A
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979	43.8	1.9	1806	18	US-10-425-115-136538	Sequence 136538,
980	43.8	1.9	1862	18	US-10-425-115-53664	Sequence 53664, A
981	43.8	1.9	2255	17	US-10-424-599-36266	Sequence 36266, A
982	43.8	1.9	513509	10	US-09-754-853A-4	Sequence 4, Appli
983	43.6	1.9	734	18	US-10-767-701-2409	Sequence 2409, Ap
984	43.6	1.9	1001	17	US-10-294-934-413	Sequence 413, App

985	43.6	1.9	1001	17	US-10-294-934-414	Sequence 414, App
986	43.6	1.9	1001	17	US-10-294-934-415	Sequence 415, App
987	43.6	1.9	1001	17	US-10-294-934-417	Sequence 417, App
988	43.6	1.9	1021	14	US-10-205-522-115	Sequence 115, App
989	43.6	1.9	1350	9	US-09-938-842A-1802	Sequence 1802, Ap
990	43.6	1.9	1350	11	US-09-938-842A-1802	Sequence 1802, Ap
991	43.6	1.9	1437	17	US-10-203-319A-47	Sequence 47, Appl
c 992	43.4	1.9	678	17	US-10-260-238-5409	Sequence 5409, Ap
993	43.4	1.9	679	18	US-10-767-701-10218	Sequence 10218, A
994	43.4	1.9	1518	18	US-10-437-963-21883	Sequence 21883, A
c 995	43.4	1.9	1929	18	US-10-437-963-10789	Sequence 10789, A
c 996	43.4	1.9	2300	18	US-10-437-963-3213	Sequence 3213, Ap
997	43.2	1.9	608	18	US-10-437-963-19715	Sequence 19715, A
998	43.2	1.9	753	18	US-10-437-963-53241	Sequence 53241, A
999	43.2	1.9	843	18	US-10-425-115-125569	Sequence 125569,
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1001	43.2	1.9	1425	18	US-10-437-963-81894	Sequence 81894, A
1002	43.2	1.9	1607	17	US-10-425-114-28586	Sequence 28586, A
1003	43.2	1.9	1636	18	US-10-425-115-76603	Sequence 76603, A
1004	43.2	1.9	10329	15	US-10-311-455-2095	Sequence 2095, Ap
1005	43.2	1.9	3673778	16	US-10-312-841-2	Sequence 2, Appli
1006	43	1.9	393	17	US-10-260-238-5737	Sequence 5737, Ap
c1007	43	1.9	1657	18	US-10-739-930-1829	Sequence 1829, Ap
1008	43	1.9	1683	17	US-10-424-599-72856	Sequence 72856, A
1009	42.8	1.8	494	18	US-10-767-701-29543	Sequence 29543, A
1010	42.8	1.8	588	18	US-10-767-701-21628	Sequence 21628, A
1011	42.8	1.8	849	18	US-10-425-115-177919	Sequence 177919,
1012	42.8	1.8	893	18	US-10-425-115-71067	Sequence 71067, A
1013	42.8	1.8	2295	17	US-10-424-599-50983	Sequence 50983, A
1016	42.6	1.8	1368	18	US-10-489-254-3	Sequence 3, Appli
c1017	42.6	1.8	1647	18	US-10-739-930-3269	Sequence 3269, Ap
1018	42.4	1.8	121	10	US-09-818-875-4016	Sequence 4016, Ap
c1019	42.4	1.8	121	10	US-09-818-875-4017	Sequence 4017, Ap
1020	42.4	1.8	121	17	US-10-209-787-4016	Sequence 4016, Ap
c1021	42.4	1.8	121	17	US-10-209-787-4017	Sequence 4017, Ap
1022	42.4	1.8	121	17	US-10-261-185-4016	Sequence 4016, Ap
c1023	42.4	1.8	121	17	US-10-261-185-4017	Sequence 4017, Ap
1024	42.4	1.8	121	18	US-10-681-074-4016	Sequence 4016, Ap
c1025	42.4	1.8	121	18	US-10-681-074-4017	Sequence 4017, Ap
1026	42.4	1.8	234	9	US-09-960-352-12264	Sequence 12264, A
1027	42.4	1.8	428	18	US-10-437-963-65973	Sequence 65973, A
c1028	42.4	1.8	747	17	US-10-424-599-137248	Sequence 137248,
1029	42.4	1.8	798	17	US-10-425-114-11594	Sequence 11594, A
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c1031	42.4	1.8	1410	17	US-10-203-319A-3	Sequence 3, Appli
1032	42.4	1.8	1410	18	US-10-489-254-2	Sequence 2, Appli
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1035	42.4	1.8	1428	11	US-09-938-842A-2381	Sequence 2381, Ap
1036	42.4	1.8	1428	17	US-10-359-369-15	Sequence 15, Appl
1037	42.4	1.8	1430	17	US-10-203-319A-13	Sequence 13, Appl
c1038	42.4	1.8	1430	17	US-10-203-319A-15	Sequence 15, Appl
1039	42.4	1.8	1437	17	US-10-424-599-40441	Sequence 40441, A
1040	42.4	1.8	1620	18	US-10-437-963-11058	Sequence 11058, A
c1041	42.4	1.8	1747	18	US-10-437-963-87975	Sequence 87975, A
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1043	42.4	1.8	2910	17	US-10-424-599-40437	Sequence 40437, A

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1045	42.4	1.8	180557	13	US-10-003-806-9	Sequence 9, Appli
1046	42.2	1.8	640	18	US-10-437-963-29554	Sequence 29554, A
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1048	42	1.8	1302	18	US-10-437-963-43996	Sequence 43996, A
1049	42	1.8	1365	18	US-10-437-963-31306	Sequence 31306, A
c1050	42	1.8	40324	18	US-10-433-793-180	Sequence 180, App
1051	41.8	1.8	795	17	US-10-424-599-128688	Sequence 128688,
1052	41.8	1.8	821	18	US-10-767-701-12684	Sequence 12684, A
1053	41.8	1.8	1494	18	US-10-437-963-6035	Sequence 6035, Ap
1054	41.8	1.8	1547	17	US-10-425-114-15608	Sequence 15608, A
1055	41.8	1.8	1591	18	US-10-425-115-8000	Sequence 8000, Ap
1056	41.8	1.8	1810	18	US-10-425-115-118492	Sequence 118492,
1057	41.6	1.8	849	18	US-10-425-115-158279	Sequence 158279,
1058	41.6	1.8	7238	15	US-10-311-455-421	Sequence 421, App
c1059	41.4	1.8	664	17	US-10-424-599-95100	Sequence 95100, A
1060	41.4	1.8	1003	17	US-10-424-599-23367	Sequence 23367, A
1061	41.4	1.8	1416	18	US-10-437-963-73968	Sequence 73968, A
1062	41.4	1.8	1434	17	US-10-203-319A-51	Sequence 51, Appl
c1063	41.4	1.8	1450	18	US-10-437-963-73966	Sequence 73966, A
1064	41.4	1.8	1637	17	US-10-425-114-4288	Sequence 4288, Ap
1065	41.4	1.8	1654	17	US-10-425-114-34899	Sequence 34899, A
1066	41.4	1.8	1730	17	US-10-425-114-26349	Sequence 26349, A
1067	41.4	1.8	1737	17	US-10-425-114-26388	Sequence 26388, A
1068	41.4	1.8	5130	18	US-10-425-115-28545	Sequence 28545, A
1069	41.2	1.8	711	18	US-10-425-115-173181	Sequence 173181,
1070	41.2	1.8	748	17	US-10-424-599-43682	Sequence 43682, A
c1071	41.2	1.8	765	17	US-10-424-599-54353	Sequence 54353, A
1072	41.2	1.8	1374	9	US-09-938-842A-1576	Sequence 1576, Ap
1073	41.2	1.8	1374	11	US-09-938-842A-1576	Sequence 1576, Ap
1074	41.2	1.8	1500	18	US-10-437-963-31808	Sequence 31808, A
c1075	41.2	1.8	1630	18	US-10-437-963-689	Sequence 689, App
1076	41.2	1.8	1648	17	US-10-424-599-131197	Sequence 131197,
1077	41.2	1.8	1693	17	US-10-424-599-139294	Sequence 139294,
1078	41.2	1.8	7829	15	US-10-311-455-1078	Sequence 1078, Ap
1079	41.2	1.8	7829	17	US-10-221-613-150	Sequence 150, App
1080	41.2	1.8	10710	15	US-10-311-455-866	Sequence 866, App
c1081	41	1.8	476	18	US-10-425-115-29545	Sequence 29545, A
1082	41	1.8	485	17	US-10-260-238-974	Sequence 974, App
c1083	41	1.8	538	17	US-10-424-599-128448	Sequence 128448,
c1084	41	1.8	99232	18	US-10-331-053-16	Sequence 16, Appl
c1085	41	1.8	99588	13	US-10-087-192-1780	Sequence 1780, Ap
1086	40.8	1.8	623	18	US-10-021-323-11890	Sequence 11890, A
1087	40.8	1.8	964	18	US-10-425-115-152977	Sequence 152977,
1088	40.8	1.8	1419	18	US-10-437-963-75846	Sequence 75846, A
1089	40.8	1.8	1485	18	US-10-437-963-44040	Sequence 44040, A
1090	40.8	1.8	1530	18	US-10-425-115-29163	Sequence 29163, A
1091	40.8	1.8	1788	18	US-10-739-930-4334	Sequence 4334, Ap
1092	40.8	1.8	2145	18	US-10-437-963-52766	Sequence 52766, A
c1093	40.8	1.8	1691139	14	US-10-067-514-1	Sequence 1, Appli
c1094	40.8	1.8	1691139	17	US-10-419-723-1	Sequence 1, Appli
1095	40.6	1.8	1684	18	US-10-425-115-58723	Sequence 58723, A
1096	40.6	1.8	3673778	16	US-10-312-841-1	Sequence 1, Appli
c1097	40.4	1.7	427	9	US-09-960-352-8924	Sequence 8924, Ap
c1098	40.4	1.7	951	18	US-10-425-115-3198	Sequence 3198, Ap
1099	40.4	1.7	1437	18	US-10-437-963-96474	Sequence 96474, A
1100	40.4	1.7	1440	18	US-10-489-254-6	Sequence 6, Appli

1101	40.4	1.7	1825	18	US-10-739-930-2896	Sequence 2896, Ap
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1103	40.2	1.7	1428	18	US-10-437-963-6034	Sequence 6034, Ap
1104	40.2	1.7	1461	18	US-10-437-963-13634	Sequence 13634, A
1105	40.2	1.7	1497	18	US-10-437-963-31876	Sequence 31876, A
c1106	40.2	1.7	1817	18	US-10-437-963-6037	Sequence 6037, Ap
1107	40	1.7	526	18	US-10-425-115-35024	Sequence 35024, A
c1108	40	1.7	745	18	US-10-437-963-20740	Sequence 20740, A
1109	40	1.7	1401	18	US-10-437-963-56917	Sequence 56917, A
1110	40	1.7	1437	18	US-10-437-963-5180	Sequence 5180, Ap
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1112	40	1.7	1524	17	US-10-425-114-16534	Sequence 16534, A
1113	40	1.7	1621	17	US-10-425-114-25554	Sequence 25554, A
1114	40	1.7	1684	18	US-10-425-115-27273	Sequence 27273, A
1115	40	1.7	1717	18	US-10-437-963-76344	Sequence 76344, A
1116	40	1.7	1926	18	US-10-425-115-71559	Sequence 71559, A
1117	40	1.7	1983	18	US-10-739-930-1013	Sequence 1013, Ap
1118	40	1.7	6029	15	US-10-311-455-1966	Sequence 1966, Ap
1119	40	1.7	7631	15	US-10-311-455-833	Sequence 833, App
1120	40	1.7	8576	15	US-10-311-455-2201	Sequence 2201, Ap
1121	40	1.7	10716	15	US-10-311-455-1391	Sequence 1391, Ap
1122	40	1.7	17389	15	US-10-311-455-1387	Sequence 1387, Ap
1123	39.8	1.7	664	13	US-10-027-632-198986	Sequence 198986,
1124	39.8	1.7	664	17	US-10-027-632-198986	Sequence 198986,
1125	39.8	1.7	697	18	US-10-767-701-8937	Sequence 8937, Ap
1126	39.8	1.7	902	18	US-10-767-701-14552	Sequence 14552, A
1127	39.8	1.7	1371	9	US-09-938-842A-1517	Sequence 1517, Ap
1128	39.8	1.7	1371	11	US-09-938-842A-1517	Sequence 1517, Ap
1129	39.8	1.7	1371	18	US-10-489-254-4	Sequence 4, Appl
1130	39.8	1.7	1407	17	US-10-260-238-1077	Sequence 1077, Ap
1131	39.8	1.7	1407	18	US-10-437-963-85974	Sequence 85974, A
1132	39.8	1.7	1437	17	US-10-203-319A-16	Sequence 16, Appl
c1133	39.8	1.7	1437	17	US-10-203-319A-18	Sequence 18, Appl
1134	39.8	1.7	1451	17	US-10-203-319A-48	Sequence 48, Appl
1135	39.8	1.7	1494	17	US-10-203-319A-54	Sequence 54, Appl
1136	39.8	1.7	1580	17	US-10-424-599-29544	Sequence 29544, A
1137	39.8	1.7	1892	17	US-10-424-599-14514	Sequence 14514, A
1138	39.8	1.7	2559	18	US-10-489-254-1	Sequence 1, Appl
c1139	39.6	1.7	563	17	US-10-424-599-43466	Sequence 43466, A
c1140	39.6	1.7	781	17	US-10-424-599-43469	Sequence 43469, A
c1141	39.6	1.7	899	17	US-10-424-599-139634	Sequence 139634,
1142	39.6	1.7	974	18	US-10-767-701-9283	Sequence 9283, Ap
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1144	39.6	1.7	1433	17	US-10-203-319A-49	Sequence 49, Appl
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1158	39.4	1.7	1540	18	US-10-425-115-143587	Sequence 143587,
1159	39.4	1.7	1837	18	US-10-425-115-64766	Sequence 64766, A
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1181	39	1.7	759	16	US-10-247-159-15	Sequence 15, Appl
1182	39	1.7	774	18	US-10-437-963-71913	Sequence 71913, A
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1214	38.8	1.7	1134	17	US-10-260-238-5631	Sequence 5631, Ap
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1219	38.8	1.7	1823	18	US-10-425-115-25921	Sequence 25921, A
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1222	38.8	1.7	7455	15	US-10-311-455-1731	Sequence 1731, Ap
1223	38.8	1.7	11049	15	US-10-311-455-642	Sequence 642, App
1224	38.8	1.7	11049	17	US-10-240-589C-28	Sequence 28, Appl
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1291	37.4	1.6	1368	11	US-09-938-842A-1384	Sequence 1384, Ap
1292	37.4	1.6	1404	9	US-09-938-842A-2210	Sequence 2210, Ap
1293	37.4	1.6	1404	11	US-09-938-842A-2210	Sequence 2210, Ap
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c1313	37	1.6	602	17	US-10-027-632-93891	Sequence 93891, A
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c1317	37	1.6	1170	10	US-09-813-432-46	Sequence 46, Appl
c1318	37	1.6	1170	17	US-10-174-364-45	Sequence 45, Appl
c1319	37	1.6	1170	17	US-10-174-364-46	Sequence 46, Appl
c1320	37	1.6	1170	17	US-10-246-583-45	Sequence 45, Appl
c1321	37	1.6	1170	17	US-10-246-583-46	Sequence 46, Appl
c1322	37	1.6	1170	18	US-10-689-832-45	Sequence 45, Appl
c1323	37	1.6	1170	18	US-10-689-832-46	Sequence 46, Appl
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c1337	37	1.6	2145	17	US-10-246-583-13	Sequence 13, Appl
c1338	37	1.6	2145	18	US-10-689-832-13	Sequence 13, Appl
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1346	37	1.6	23934	9	US-09-764-877-2544	Sequence 2544, Ap
c1347	37	1.6	23934	10	US-09-764-891-7210	Sequence 7210, Ap
1348	37	1.6	23934	14	US-10-074-095-777	Sequence 777, App
1349	37	1.6	23934	17	US-10-212-872-777	Sequence 777, App
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1351	37	1.6	23934	17	US-10-242-515-2544	Sequence 2544, Ap
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1359	36.8	1.6	697	17	US-10-424-599-52324	Sequence 52324, A
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1363	36.8	1.6	1001	17	US-10-294-934-382	Sequence 382, App
1364	36.8	1.6	1041	9	US-09-916-790-3	Sequence 3, Appli
1365	36.8	1.6	1041	17	US-10-678-786-3	Sequence 3, Appli
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1368	36.8	1.6	1275	13	US-10-016-985-1	Sequence 1, Appli
1369	36.8	1.6	1275	18	US-10-473-144-7	Sequence 7, Appli
1370	36.8	1.6	1282	18	US-10-322-281-37	Sequence 37, Appli
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1372	36.8	1.6	1473	13	US-10-016-985-3	Sequence 3, Appli
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1375	36.8	1.6	1829	10	US-09-876-997-238	Sequence 238, App
1376	36.8	1.6	1874	15	US-10-180-375-127	Sequence 127, App
1377	36.8	1.6	1874	17	US-10-183-687-143	Sequence 143, App
1378	36.8	1.6	1982	18	US-10-473-144-9	Sequence 9, Appli
1379	36.8	1.6	2060	17	US-10-288-798-25	Sequence 25, Appli
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1385	36.8	1.6	2893	9	US-09-916-790-1	Sequence 1, Appli
1386	36.8	1.6	2893	17	US-10-678-786-1	Sequence 1, Appli
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1389	36.8	1.6	9997	15	US-10-240-485-38	Sequence 38, Appli
1390	36.8	1.6	10254	15	US-10-311-455-1048	Sequence 1048, Ap
1391	36.8	1.6	12393	15	US-10-311-455-1235	Sequence 1235, Ap
1392	36.8	1.6	17421	14	US-10-239-676-54	Sequence 54, Appli
1393	36.8	1.6	17421	15	US-10-240-453-56	Sequence 56, Appli
1394	36.8	1.6	34688	18	US-10-433-793-89	Sequence 89, Appli
1395	36.8	1.6	73334	15	US-10-311-455-2098	Sequence 2098, Ap
1396	36.8	1.6	73334	17	US-10-240-589C-128	Sequence 128, App
1397	36.6	1.6	324	18	US-10-437-963-91462	Sequence 91462, A
1398	36.6	1.6	363	18	US-10-437-963-44337	Sequence 44337, A
1399	36.6	1.6	667	18	US-10-767-701-3793	Sequence 3793, Ap
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1406	36.6	1.6	3401	18	US-10-370-715B-153	Sequence 153, App
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1431	36.4	1.6	8675	18	US-10-804-677-18	Sequence 18, Appl
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1438	36.4	1.6	1790242	18	US-10-719-993-6940	Sequence 6940, Ap
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1463	36.2	1.6	11122	11	US-09-984-429-444	Sequence 444, App
1464	36.2	1.6	11172	9	US-09-764-878-231	Sequence 231, App
1465	36.2	1.6	11172	14	US-10-079-854-231	Sequence 231, App
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